

SEQUENCE LISTING

<110> Micromet AG

<120> Multispecific deimmunized CD3 binders

<130> G 2728 PCT

<160> 409

<170> PatentIn version 3.1

<210> 1

<211> 729

<212> DNA

<213> artificial sequence

<220>

<223> wt Anti-CD3 cassette

<400> 1

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cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac	180
aatcagaagt tcaaggacaa ggccacattg actacagaca aatcctccag cacagcctac	240
atgcaactga gcagcctgac atctgaggac tctgcagtct attactgtgc aagatattat	300
gatgatcatt actgccttga ctactggggc caaggcacca ctctcacagt ctctcagtc	360
gaagggtgaa gtggagggtc tgggtggaagt ggagggtcag gtggagtcga cgacattcag	420
ctgaccagct ctccagcaat catgtctgca tctccagggg agaaggtcac catgacctgc	480
agagccagtt caagtgtgaa ttacatgaac tggtagcagc agaagtcagg cacctccccc	540
aaaagatgga tttatgacac atccaaagtg gcttctggag tcccttatcg cttcagtggc	600
agtgggtctg ggacctcata ctctctcaca atcagcagca tggaggctga agatgctgcc	660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtgctgg gaccaagctg	720
gagctgaaa	729

<210> 2

<211> 243

<212> PRT

<213> artificial sequence

<220>

<223> wt Anti-CD3 cassette

<400> 2

Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala

1	5	10	15														
Ser	Val	Lys	Met	Ser	Cys	Lys	Thr	Ser	Gly	Tyr	Thr	Phe	Thr	Arg	Tyr		
			20					25					30				
Thr	Met	His	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile		
		35					40					45					
Gly	Tyr	Ile	Asn	Pro	Ser	Arg	Gly	Tyr	Thr	Asn	Tyr	Asn	Gln	Lys	Phe		
	50					55				60							
Lys	Asp	Lys	Ala	Thr	Leu	Thr	Thr	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr		
65					70					75					80		
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys		
				85					90					95			
Ala	Arg	Tyr	Tyr	Asp	Asp	His	Tyr	Cys	Leu	Asp	Tyr	Trp	Gly	Gln	Gly		
			100					105					110				
Thr	Thr	Leu	Thr	Val	Ser	Ser	Val	Glu	Gly	Gly	Ser	Gly	Gly	Ser	Gly		
		115					120					125					
Gly	Ser	Gly	Gly	Ser	Gly	Gly	Val	Asp	Asp	Ile	Gln	Leu	Thr	Gln	Ser		
	130					135					140						
Pro	Ala	Ile	Met	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys		
145					150					155					160		
Arg	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Ser		
				165					170					175			
Gly	Thr	Ser	Pro	Lys	Arg	Trp	Ile	Tyr	Asp	Thr	Ser	Lys	Val	Ala	Ser		
			180					185					190				
Gly	Val	Pro	Tyr	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser		
		195					200					205					
Leu	Thr	Ile	Ser	Ser	Met	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys		
	210					215						220					
Gln	Gln	Trp	Ser	Ser	Asn	Pro	Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu		
225					230					235					240		

Glu Leu Lys

<210> 3
 <211> 18
 <212> PRT
 <213> artificial sequence

<220>
 <223> deimmunized linker

<400> 3

Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
 1 5 10 15

Ala Asp

<210> 4
 <211> 729
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH2/VL1

<400> 4
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 cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 180
 gcacagaagt tgcagggccg cgtcacaatg actacagaca cttccaccag cacagcctac 240
 atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc 360
 gaaggtacta gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacattcag 420
 atgacccagt ctccatctag cctgtctgca tctgtcgggg accgtgtcac catcacctgc 480
 agagccagtc aaagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
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 gagatcaaa 729

<210> 5

<211> 243
 <212> PRT
 <213> artificial sequence

<220>
 <223> VH2/VL1

<400> 5

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ala Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu
 50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser
 130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
 145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys

<210> 6
 <211> 729
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH2/VL2

<400> 6
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 cctggacagg gtctggaatg gattggatac attaattcta gccgtgggta tactaattac 180
 gcacagaagt tgcagggccg cgtcacaatg actacagaca cttccaccag cacagcctac 240
 atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
 gaaggctacta gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacattgta 420
 ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480
 agagccagtc aaagtgtaag ttacatgaac tggtaaccagc agaagccggg caaggcaccc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
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 gagatcaaa 729

<210> 7
 <211> 243
 <212> PRT
 <213> artificial sequence

<220>
 <223> VH2/VL2

<400> 7

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ala Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu
50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys

<210> 8

<211> 729

<212> DNA

<213> artificial sequence

<220>

<223> VH2/VL3

<400> 8

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cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac      180
gcacagaagt tgcagggccg cgtcacaatg actacagaca cttccaccag cacagcctac      240
atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat      300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc      360
gaagggtacta gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacattgta      420
ctgaccacgt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgacctgc      480
agagccagtt caagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc      540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc      600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc      660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcgggtggcgg gaccaagggtg      720
gagatcaaa                                     729

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<210> 9

<211> 243

<212> PRT

<213> artificial sequence

<220>

<223> VH2VL3

<400> 9

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Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1           5           10           15

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```

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ala Thr Arg Tyr
20           25           30

```

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu
 50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
 145 150 155 160

Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys

<210> 10
 <211> 729

<212> DNA
 <213> artificial sequence

<220>
 <223> VH3/VL1

<400> 10
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 cctggacagg gtctggaatg gattggatac attaataccta gccgtgggta tactaattac 180
 gcacagaagt tgcagggccg cgtcacaatg actacagaca cttccaccag cacagcctac 240
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 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
 gaaggtacta gtactggttc tgggtggaagt ggagggttcag gtggagcaga cgacattcag 420
 atgacccagt ctccatctag cctgtctgca tctgtcggg accgtgtcac catcacctgc 480
 agagccagtc aaagtgtaag ttacatgaac tggtagcagc agaagccggg caaggcaccc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tcctgtctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
 acttattact gccaacagtg gagtagtaac ccgctcacgt tcgggtggcgg gaccaaggtg 720
 gagatcaaa 729

<210> 11
 <211> 243
 <212> PRT
 <213> artificial sequence

<220>
 <223> VH3/VL1

<400> 11

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ala Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu
 50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser
130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys

<210> 12

<211> 729

<212> DNA

<213> artificial sequence

<220>

<223> VH3/VL2

<400> 12

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cctggacagg gtctggaatg gattggatac attaataccta gccgtgggta tactaattac    180
gcacagaagt tgcagggccg cgtcacaaatg actacagaca cttccaccag cacagcctac    240
ctgcaaataa acagcctgaa aactgaggac actgcagtct attactgtgc aagatattat    300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcttcaggc    360
gaaggtaact gtactgggtc tgggtggaagt ggagggttcag gtggagcaga cgacattgta    420
ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc    480
agagccagtc aaagtgtaag ttacatgaac tggtagcagc agaagccggg caaggcagcc    540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccttgctcg cttcagtggc    600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc    660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg    720
gagatcaaa                                     729

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<210> 13
<211> 243
<212> PRT
<213> artificial sequence

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<220>
<223> VH3/VL2

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<400> 13

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Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1           5           10           15

```

```

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ala Thr Arg Tyr
          20           25           30

```

```

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
          35           40           45

```

```

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu
          50           55           60

```

```

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
          65           70           75           80

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```

Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys
          85           90           95

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Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys

<210> 14
 <211> 729
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH3/VL3

<400> 14
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 cctggacagg gtctggaatg gattggatac attaactcta gccgtgggta tactaattac 180
 gcacagaagt tgcagggccg cgtcacaatg actacagaca cttccaccag cacagcctac 240
 ctgcaaataa acagcctgaa aactgaggac actgcagtct attactgtgc aagatattat 300

gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
gaaggtacta gtactggttc tgggtggaagt ggaggttcag gtggagcaga cgacattgta 420
ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgacctgc 480
agagccagtt caagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg 720
gagatcaaa 729

<210> 15
<211> 243
<212> PRT
<213> artificial sequence

<220>
<223> VH3/VL3

<400> 15

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ala Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu
50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
 145 150 155 160

Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys

<210> 16
 <211> 729
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH5/VLI

<400> 16
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 cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 180
 gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240
 atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
 gaaggtacta gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacattcag 420
 atgacccagt ctccatctag cctgtctgca tctgtcgggg accgtgtcac catcacctgc 480
 agagccagtc aaagtgtgaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540

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aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc      600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc      660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg      720
gagatcaaa                                         729

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<210> 17
<211> 243
<212> PRT
<213> artificial sequence

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<220>
<223> VH5/VL1

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<400> 17

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Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1              5              10              15

```

```

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
      20              25              30

```

```

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
      35              40              45

```

```

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
      50              55              60

```

```

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
      65              70              75              80

```

```

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
      85              90              95

```

```

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
      100              105              110

```

```

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
      115              120              125

```

```

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser
      130              135              140

```

```

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
      145              150              155              160

```

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys

<210> 18
 <211> 729
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH5/VL2

<400> 18
 gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaaggtg 60
 tcttgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120
 cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 180
 gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240
 atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
 gaaggtacta gtactgggtc tgggtggaagt ggagggtcag gtggagcaga cgacattgta 420
 ctgaccaggt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480
 agagccagtc aaagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
 acttattact gccaacagtg gagtagtaac ccgctcacgt tcgggtggcgg gaccaaggtg 720
 gagatcaaa 729

<210> 19
 <211> 243
 <212> PRT
 <213> artificial sequence

<220>
 <223> VH5/VL2

<400> 19

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys

<210> 20
 <211> 729
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH5/VL3

<400> 20
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 tcttgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120
 cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 180
 gcagacagcg tcaagggcgc cttcacaatc actacagaca aatccaccag cacagcctac 240
 atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
 gaagggtacta gtactgggtc tgggtggaagt ggagggtcag gtggagcaga cgacattgta 420
 ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgacctgc 480
 agagccagtt caagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tcctgtctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
 acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaagggtg 720
 gagatcaaa 729

<210> 21
 <211> 243
 <212> PRT
 <213> artificial sequence

<220>

<223> VH5/VL3

<400> 21

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
 145 150 155 160

Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys

<210> 22
 <211> 729
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH7/VL1

<400> 22
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 tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120
 cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 180
 aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac 240
 atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc 360
 gaaggtacta gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacattcag 420
 atgacccagt ctccatctag cctgtctgca tctgtcgggg accgtgtcac catcacctgc 480
 agagccagtc aaagtgtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
 acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg 720
 gagatcaaa 729

<210> 23
 <211> 243
 <212> PRT
 <213> artificial sequence

<220>
 <223> VH7/VL1

<400> 23

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser
130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys

<210> 24
 <211> 729
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH7/VL2

<400> 24
 gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg 60
 tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120
 cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 180
 aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac 240
 atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc 360
 gaaggtacta gtactggttc tggtggaagt ggagggtcag gtggagcaga cgacattgta 420
 ctgaccagtc ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480
 agagccagtc aaagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcacc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
 acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaagggtg 720
 gagatcaaa 729

<210> 25
 <211> 243
 <212> PRT
 <213> artificial sequence

<220>
 <223> VH7/VL2

<400> 25

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
 50 55 60

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys

<210> 26

<211> 729

<212> DNA

<213> artificial sequence

<220>

<223> VH7/VL3

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<400> 26
gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg      60
tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca      120
cctggacagg gtctggaatg gattggatac attaataccta gccgtgggta tactaattac      180
aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac      240
atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat      300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc      360
gaaggctacta gtactggttc tgggtggaagt ggaggttcag gtggagcaga cgacattgta      420
ctgaccaggt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgacctgc      480
agagccagtt caagtgtgaa ttacatgaac tggtaaccagc agaagccggg caaggcaccc      540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc      600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc      660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcgggtggcgg gaccaagggtg      720
gagatcaaa                                     729

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<210> 27
<211> 243
<212> PRT
<213> artificial sequence

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<220>
<223> VH7/VL3

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```

<400> 27

```

```

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1           5           10           15

```

```

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20           25           30

```

```

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35           40           45

```

```

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
50           55           60

```

```

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65           70           75           80

```

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
 145 150 155 160

Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys

<210> 28

<211> 20

<212> DNA

<213> artificial sequence

<220>

<223> Sequencing primer

<400> 28

cctcagacag tggttcaaag

20

<210> 29

<211> 18

<212> DNA

<213> artificial sequence

<220>

<223> Sequencing primer

<400> 29

agccgccacg tgggcctc

18

<210> 30

<211> 1473

<212> DNA

<213> artificial sequence

<220>

<223> anti-CD3 VH5/VL2 x 3-1 VHVL

<400> 30

gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaaggtg	60
tcttgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca	120
cctggacagg gtctggaatg gattggatac attaataccta gccgtgggta tactaattac	180
gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac	240
atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat	300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc	360
gaagg tacta gtactgggtc tgggtggaagt ggagggtcag gtggagcaga cgacattgta	420
ctgaccagtc ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc	480
agagccagtc aaagtgtgaa ttacatgaac tgggtaccagc agaagccggg caaggcaccc	540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc	600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc	660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcgggtggcgg gaccaaggtg	720
gagatcaaat ccggagggtg tggatccgag gtgcagctgc tcgagcagtc tggagctgag	780
ctggtgaaac ctggggcctc agtgaagata tcttgcaagg cttctggata cgccttcact	840
aactactggc taggttgggt aaagcagagg cctggacatg gacttgagtg gattggagat	900
cttttcctg gaagtggtaa tactcactac aatgagaggt tcaggggcaa agccacactg	960
actgcagaca aatcctcgag cacagccttt atgcagctca gtagcctgac atctgaggac	1020
tctgctgtct atttctgtgc aagattgagg aactgggacg aggctatgga ctactggggc	1080
caagggacca cggtcaccgt ctctcagggt ggtggtggtt ctggcggcgg cggctccggt	1140
ggtggtggtt ctgagctcgt catgaccagc tctccatctt atcttgctgc atctcctgga	1200
gaaaccatta ctattaattg cagggcaagt aagagcatta gcaaatattt agcctggtat	1260

caagagaaac ctgggaaaac taataagctt cttatctact ctggatccac tttgcaatct 1320
 ggaattccat caaggttcag tggcagtgga tctggtacag atttcactct caccatcagt 1380
 agcctggagc ctgaagattt tgcaatgtat tactgtcaac agcataatga atatccgtac 1440
 acgttcggag gggggaccaa gcttgagatc aaa 1473

<210> 31
 <211> 491
 <212> PRT
 <213> artificial sequence

<220>
 <223> anti-CD3 VH5/VL2 x 3-1 VHVL
 <400> 31

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln
 245 250 255

Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys
 260 265 270

Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Trp Leu Gly Trp Val Lys
 275 280 285

Gln Arg Pro Gly His Gly Leu Glu Trp Ile Gly Asp Leu Phe Pro Gly
 290 295 300

Ser Gly Asn Thr His Tyr Asn Glu Arg Phe Arg Gly Lys Ala Thr Leu
 305 310 315 320

Thr Ala Asp Lys Ser Ser Ser Thr Ala Phe Met Gln Leu Ser Ser Leu
 325 330 335

Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Leu Arg Asn Trp
 340 345 350

Asp Glu Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 355 360 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 370 375 380

Glu Leu Val Met Thr Gln Ser Pro Ser Tyr Leu Ala Ala Ser Pro Gly
 385 390 395 400

Glu Thr Ile Thr Ile Asn Cys Arg Ala Ser Lys Ser Ile Ser Lys Tyr
 405 410 415

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Thr Asn Lys Leu Leu Ile
 420 425 430

Tyr Ser Gly Ser Thr Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
 435 440 445

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 450 455 460

Glu Asp Phe Ala Met Tyr Tyr Cys Gln Gln His Asn Glu Tyr Pro Tyr
 465 470 475 480

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 485 490

<210> 32

<211> 1500

<212> DNA

<213> artificial sequence

<220>

<223> anti-CD3 VH5/VL2 x 4-7 VHVL

<400> 32

gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg	60
tcttgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca	120
cctggacagg gtctggaatg gattggatac attaattcta gccgtgggta tactaattac	180
gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac	240
atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat	300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc	360
gaaggtaacta gtactgggtc tgggtggaagt ggagggttcag gtggagcaga cgacattgta	420
ctgaccacagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc	480
agagccagtc aaagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc	540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc	600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc	660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcgggtggcgg gaccaagggtg	720

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gagatcaaat ccggaggtgg tggatccgag gtgcagctgc tcgagcagtc tggagctgag      780
ctggcgaggc ctggggcttc agtgaagctg tcctgcaagg cttctggcta caccttcaca      840
aactatggtt taagctgggt gaagcagagg cctggacagg tccttgagtg gattggagag      900
gtttatccta gaattggtaa tgcttactac aatgagaagt tcaagggcaa ggccacactg      960
actgcagaca aatcctccag cacagcgtcc atggagctcc gcagcctgac ctctgaggac     1020
tctgcggtct atttctgtgc aagacgggga tcctacgata ctaactacga ctggtacttc     1080
gatgtctggg gccaaaggac cacggtcacc gtctcctcag gtggtggtgg ttctggcggc     1140
ggcggctccg gtggtggtgg ttctgagctc gtgatgacc agactccact ctccctgcct     1200
gtcagtcttg gagatcaagc ctccatctct tgcagatcta gtcagagcct tgtacacagt     1260
aatggaaaca cctatttaca ttggtacctg cagaagccag gccagtctcc aaagctcctg     1320
atctacaaag tttccaaccg attttctggg gtcccagaca ggttcagtgg cagtggatca     1380
gggacagatt tcacactcaa gatcagcaga gtggaggctg aggatctggg agtttatttc     1440
tgctctcaaa gtacacatgt tccgtacacg ttcggagggg ggaccaagct tgagatcaaa     1500

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<210> 33

<211> 500

<212> PRT

<213> artificial sequence

<220>

<223> anti-CD3 VH5/VL2 x 4-7 VHVL

<400> 33

```

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1           5           10          15

```

```

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20           25           30

```

```

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35           40           45

```

```

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
50           55           60

```

```

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65           70           75           80

```

```

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85           90           95

```

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln
 245 250 255

Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys
 260 265 270

Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys
 275 280 285

Gln Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg
 290 295 300

Ile Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu
 305 310 315 320

Thr Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu

325

330

335

Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr
 340 345 350

Asp Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr
 355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380

Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu Pro
 385 390 395 400

Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
 405 410 415

Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys
 420 425 430

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
 435 440 445

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
 450 455 460

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe
 465 470 475 480

Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys
 485 490 495

Leu Glu Ile Lys
 500

<210> 34
 <211> 1500
 <212> DNA
 <213> artificial sequence

<220>
 <223> anti-CD3 VH5/VL2 x 4-7 VLVH

<400> 34
 gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg 60
 tcttgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120

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cctggacagg gtctggaatg gattggatac attaataccta gccgtgggta tactaattac 180
gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240
atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
gaaggtacta gtactgggtc tgggtggaagt ggagggttcag gtggagcaga cgacattgta 420
ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480
agagccagtc aaagtgtaag ttacatgaac tggtagcagc agaagccggg caaggcaccc 540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaagggtg 720
gagatcaaat ccggagggtg tggatccgag ctctgtgatga cccagactcc actctccctg 780
cctgtcagtc ttggagatca agcctccatc tcttgagat ctagtcagag ccttgtagac 840
agtaatggaa acacctatctt acattgggtac ctgcagaagc caggccagtc tccaaagctc 900
ctgatctaca aagtttccaa ccgattttct ggggtcccag acagggttcag tggcagtggg 960
tcagggacag atttcacact caagatcagc agagtggagg ctgaggatct gggagtttat 1020
ttctgctctc aaagtacaca tgttccgtac acgttcggag gggggaccaa gcttgagatc 1080
aaagggtggtg gtggttctgg cggcggcggc tccggtggtg gtggttctga ggtgcagctg 1140
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gcttctggct acaccttcac aaactatggt ttaagctggg tgaagcagag gcctggacag 1260
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ttcaagggca aggccacact gactgcagac aaatcctcca gcacagcgtc catggagctc 1380
cgcagcctga cctctgagga ctctgcggtc tatttctgtg caagacgggg atcctacgat 1440
actaactacg actggtactt cgatgtctgg ggccaaggga ccacggtcac cgtctcctca 1500

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<210> 35

<211> 500

<212> PRT

<213> artificial sequence

<220>

<223> anti-CD3 VH5/VL2 x 4-7 VLVH

<400> 35

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

1	5	10	15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr	20	25	30
Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile	35	40	45
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val	50	55	60
Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr	65	70	75
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys	85	90	95
Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly	100	105	110
Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly	115	120	125
Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser	130	135	140
Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys	145	150	155
Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro	165	170	175
Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser	180	185	190
Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser	195	200	205
Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys	210	215	220
Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val	225	230	235
			240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr
 245 250 255

Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys
 260 265 270

Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His
 275 280 285

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys
 290 295 300

Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
 305 310 315 320

Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp
 325 330 335

Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe
 340 345 350

Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly
 355 360 365

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser
 370 375 380

Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys
 385 390 395 400

Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln
 405 410 415

Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile
 420 425 430

Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr
 435 440 445

Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr
 450 455 460

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp
 465 470 475 480

Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val
 485 490 495

Thr Val Ser Ser
 500

<210> 36
 <211> 1491
 <212> DNA
 <213> artificial sequence

<220>
 <223> anti-CD3 VH5/VL2 x 5-10 VHVL

<400> 36
 gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaaggtg 60
 tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120
 cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 180
 gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240
 atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctccctcaggc 360
 gaagggtacta gtactgggtc tgggtggaagt ggagggttcag gtggagcaga cgacattgta 420
 ctgaccocagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480
 agagccagtc aaagtgtgaa ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
 acttattact gccaacagtg gagtagtaac ccgctcacgt tcgggtggcgg gaccaaggtg 720
 gagatcaaat ccggagggtg tggatccgag gtgcagctgc tcgagcagtc tggagctgag 780
 ctggtgaaggc ctgggacttc agtgaagata tcctgcaagg cttctggata cgccttcact 840
 aactactggc taggttgggt aaagcagagg cctggacatg gacttgagtg gattggagat 900
 attttccctg gaagtggtaa tatccactac aatgagaagt tcaagggcaa agccacactg 960
 actgcagaca aatcttcgag cacagcctat atgcagctca gtagcctgac atttgaggac 1020
 tctgctgtct atttctgtgc aagactgagg aactgggacg agcctatgga ctactggggc 1080
 caagggacca cggtcaccgt ctccctcagg ggtgggtggt ctggcggcgg cggctccggt 1140
 ggtgggtggt ctgagctcgt gatgacacag tctccatcct ccctgactgt gacagcagga 1200
 gagaaggtca ctatgagctg caagtccagt cagagtctgt taaacagtgg aaatcaaaag 1260

aactacttga cctggtacca gcagaaacca gggcagcctc ctaaactgtt gatctactgg 1320
 gcatccacta gggaatctgg ggtccctgat cgcttcacag gcagtggatc tggaacagat 1380
 ttcactctca ccatcagcag tgtgcaggct gaagacctgg cagtttatta ctgtcagaat 1440
 gattatagtt atccgctcac gttcgggtgct gggaccaagc ttgagatcaa a 1491

<210> 37

<211> 497

<212> PRT

<213> artificial sequence

<220>

<223> anti-CD3 VH5/VL2 x 5-10 VHVL

<400> 37

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln
 245 250 255

Ser Gly Ala Glu Leu Val Arg Pro Gly Thr Ser Val Lys Ile Ser Cys
 260 265 270

Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Trp Leu Gly Trp Val Lys
 275 280 285

Gln Arg Pro Gly His Gly Leu Glu Trp Ile Gly Asp Ile Phe Pro Gly
 290 295 300

Ser Gly Asn Ile His Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu
 305 310 315 320

Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu
 325 330 335

Thr Phe Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Leu Arg Asn Trp
 340 345 350

Asp Glu Pro Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 355 360 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 370 375 380

Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
 385 390 395 400

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
 405 410 415

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
 420 425 430

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 435 440 445

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 450 455 460

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
 465 470 475 480

Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
 485 490 495

Lys

<210> 38

<211> 1491

<212> DNA

<213> artificial sequence

<220>

<223> anti-CD3 VH5/VL2 x 5-10 VLVH

<400> 38

gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg	60
tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca	120
cctggacagg gtctggaatg gattggatac attaataccta gccgtgggta tactaattac	180
gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac	240
atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat	300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc	360
gaagggtacta gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacattgta	420
ctgaccagtc ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc	480
agagccagtc aaagtgtgaa ttacatgaac tgggtaccagc agaagccggg caaggcacc	540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc	600

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agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg 720
gagatcaaat ccggaggtgg tggatccgag ctctgtgatga cacagtctcc atcctccctg 780
actgtgacag caggagagaa ggtcactatg agctgcaagt ccagtcagag tctgttaaac 840
agtggaaatc aaaagaacta cttgacctgg taccagcaga aaccagggca gcctcctaaa 900
ctgttgatct actgggcac cactagggaa tctgggggtcc ctgatcgctt cacaggcagt 960
ggatctggaa cagatttcac tctcaccatc agcagtgtgc aggctgaaga cctggcagtt 1020
tattactgtc agaatgatta tagttatccg ctacagttcg gtgctgggac caagcttgag 1080
atcaaaggtg gtggtggttc tggcggcggc ggctccggtg gtggtggttc tgaggtgcag 1140
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aaggcttctg gatacgctt cactaactac tggctaggtt gggtaaagca gaggcctgga 1260
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aagttcaagg gcaaagccac actgactgca gacaaatctt cgagcacagc ctatatgcag 1380
ctcagtagcc tgacatttga ggactctgct gtctatttct gtgcaagact gaggaactgg 1440
gacgagccta tggactactg gggccaaggg accacggtca ccgtctctc a 1491

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<210> 39

<211> 497

<212> PRT

<213> artificial sequence

<220>

<223> anti-CD3 VH5/VL2 x 5-10 VLVH

<400> 39

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Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1           5           10           15

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```

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20           25           30

```

```

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35           40           45

```

```

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
50           55           60

```

```

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65           70           75           80

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Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser
 245 250 255

Pro Ser Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys
 260 265 270

Lys Ser Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu
 275 280 285

Thr Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
 290 295 300

Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser

305 310 315 320
 Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu
 325 330 335
 Asp Leu Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr
 340 345 350
 Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly
 355 360 365
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln
 370 375 380
 Ser Gly Ala Glu Leu Val Arg Pro Gly Thr Ser Val Lys Ile Ser Cys
 385 390 395 400
 Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Trp Leu Gly Trp Val Lys
 405 410 415
 Gln Arg Pro Gly His Gly Leu Glu Trp Ile Gly Asp Ile Phe Pro Gly
 420 425 430
 Ser Gly Asn Ile His Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu
 435 440 445
 Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu
 450 455 460
 Thr Phe Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Leu Arg Asn Trp
 465 470 475 480
 Asp Glu Pro Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 485 490 495

Ser

<210> 40

<211> 35

<212> DNA

<213> artificial sequence

<220>

<223> DI anti-CD3 K52VHBsrGI

<400> 40
agggtgtacac tccgacgtcc aactggtgca gtcag 35

<210> 41
<211> 30
<212> DNA
<213> artificial sequence

<220>
<223> DI anti-CD3 52VLBspEI

<400> 41
aatccggatt tgatctccac cttggtcccg 30

<210> 42
<211> 51
<212> DNA
<213> artificial sequence

<220>
<223> 4-7 VH GS15 FOR

<400> 42
ggcggcgggcg gctccggtgg tgggtggttct gaggtgcagc tgctcgagca g 51

<210> 43
<211> 53
<212> DNA
<213> artificial sequence

<220>
<223> 4-7 VH SalI REV

<400> 43
ttttaagtcg acctaagat gatgatgatg atgtgaggag acggtgaccg tgg 53

<210> 44
<211> 49
<212> DNA
<213> artificial sequence

<220>
<223> 510VLBspEI

<400> 44
ctgaaatccg gaggtggtgg atccgagctc gtgatgacac agtctccat 49

<210> 45
<211> 53
<212> DNA
<213> artificial sequence

<220>
<223> 510VLGS15REV

<400> 45
ggagccgccc cgcgcagaac caccaccacc ttgatctca agcttggtcc cag 53

<210> 46
<211> 49
<212> DNA
<213> artificial sequence

<220>
<223> 510VHGS15

<400> 46
ggcggcggcg gctccggtgg tgggtggttct gaggtgcagc tgctcgagc 49

<210> 47
<211> 53
<212> DNA
<213> artificial sequence

<220>
<223> 510VHSalIREV

<400> 47
ttttaagtcg acctaataat gatgatgatg atgtgaggag acggtgaccg tgg 53

<210> 48
<211> 1518
<212> DNA
<213> artificial sequence

<220>
<223> 3-1(VL-VH)xanti-CD3(VH(5)-VL(2))

<400> 48
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt aactccgag 60
ctcgtcatga cccagtcctc atcttatctt gctgcatctc ctggagaaac cattactatt 120
aattgcaggg caagtaagag cattagcaaa tatttagcct ggtatcaaga gaaacctggg 180
aaaactaata agcttcttat ctactctgga tccactttgc aatctggaat tccatcaagg 240
ttcagtggca gtggatctgg tacagatttc actctcacca tcagtagcct ggagcctgaa 300
gattttgcaa tgtattactg tcaacagcat aatgaatatc cgtacacgtt cggagggggg 360
accaagcttg agatcaaagg tgggtggtgg tctggcggcg gcggctccgg tgggtggtgg 420
tctgaggtgc agctgctcga gcagtctgga gctgagctgg tgaaacctgg ggcctcagtg 480
aagatatcct gcaaggcttc tggatacgcc ttcactaact actggctagg ttgggtaaag 540
cagaggcctg gacatggact tgagtggatt ggagatcttt tccctggaag tggttaatact 600
cactacaatg agaggttcag gggcaaagcc aactgactg cagacaaatc ctcgagcaca 660


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gcctttatgc agctcagtag cctgacatct gaggactctg ctgtctatct ctgtgcaaga 720
ttgaggaact gggacgaggg tatggactac tggggccaag ggaccacggg caccgtctcc 780
tccggaggtg gtggctccga cgtccaactg gtgcagtcag gggctgaagt gaaaaaacct 840
ggggcctcag tgaagggtgtc ctgcaaggct tctggctaca cttttactag gtacacgatg 900
cactgggtaa ggcaggcacc tggacagggt ctggaatgga ttggatacat taatcctagc 960
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tccaccagca cagcctacat ggaactgagc agcctgcgtt ctgaggacac tgcaacctat 1080
tactgtgcaa gatattatga tgatcattac tgccttgact actggggcca aggcaaccag 1140
gtcacogtct cctcaggcga aggtactagt actgggtctg gaggttcagg tggagcagac 1200
gacattgtac tgaccocagtc tccagcaact ctgtctctgt ctccagggga gcgtgccacc 1260
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aaggcaccca aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 1380
ttcagtgcca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 1440
gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cggtggcggg 1500
accaaggtgg agatcaaa 1518

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<210> 49
<211> 506
<212> PRT
<213> artificial sequence

<220>
<223> 3-1(VL-VH)xanti-CD3(VH(5)-VL(2))

<400> 49

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Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1           5           10           15

```

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Val His Ser Glu Leu Val Met Thr Gln Ser Pro Ser Tyr Leu Ala Ala
20           25           30

```

```

Ser Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala Ser Lys Ser Ile
35           40           45

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Ser Lys Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Thr Asn Lys
50           55           60

```

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Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly Ile Pro Ser Arg

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65		70		75		80
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser	85		90		95	
Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln Gln His Asn Glu	100		105		110	
Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly	115		120		125	
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln	130		135		140	
Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val	145		150		155	160
Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Trp Leu	165		170		175	
Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile Gly Asp	180		185		190	
Leu Phe Pro Gly Ser Gly Asn Thr His Tyr Asn Glu Arg Phe Arg Gly	195		200		205	
Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Phe Met Gln	210		215		220	
Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg	225		230		235	240
Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr	245		250		255	
Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val Gln	260		265		270	
Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys	275		280		285	
Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg	290		295		300	

Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser
 305 310 315 320

Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile
 325 330 335

Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu
 340 345 350

Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp
 355 360 365

His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 370 375 380

Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ala Asp
 385 390 395 400

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 405 410 415

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
 420 425 430

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
 435 440 445

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 450 455 460

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
 465 470 475 480

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
 485 490 495

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 500 505

<210> 50

<211> 60

<212> DNA

<213> artificial sequence

<220>

<223> Me83

<400> 50
ggttctggcg gcggcggctc cgggtggtggt ggttctgagg tgcagctgct cgacagtctg 60

<210> 51
<211> 41
<212> DNA
<213> artificial sequence

<220>
<223> Me84

<400> 51
gtgctccgga ggagacggtg acögtggtcc cttggcccca g 41

<210> 52
<211> 53
<212> DNA
<213> artificial sequence

<220>
<223> Me90

<400> 52
ccggagccgc cgccgccaga accaccacca cctttgatct caagcttggt ccc 53

<210> 53
<211> 52
<212> DNA
<213> artificial sequence

<220>
<223> Me91a

<400> 53
ggattgtaca ctccgagctc gtcattgaccc agtctccatc ttatcttgct gc 52

<210> 54
<211> 1560
<212> DNA
<213> artificial sequence

<220>
<223> 3-5(VL-VH)xanti-CD3 (VH(5)-VL(2))

<400> 54
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt acactccgcg 60
cgcgagctcg tgatgaccca gactccactc tccctgcctg tcagtcttg agatcaagcc 120
tccatctctt gcagatctag tcagagcctt gtacacagta atggaaacac ctatttacat 180
tggtacctgc agaagccagg ccagtctcca aagctcctga tctacaaagt ttccaaccga 240
ttttctgggg tcccagacag gttcagtggc agtggatcag ggacagattt cacactcaag 300

```

atcagcagag tggaggctga ggatctggga gtttatttct gctctcaaag tacacatggt 360
ccgtacacgt tcggaggggg gaccaagctt gagatcaaag gtggtggtgg ttctggcggc 420
ggcgggtccg gtggtggtgg ttctgaggtg cagctgctcg agcagtctgg agctgagctg 480
gtaaggcctg ggacttcagt gaagctgtcc tgcaaggctt ctggctacac cttcacaagc 540
tatggtttaa gctgggtgaa gcagagaact ggacagggcc ttgagtggat tggagaggtt 600
tattctagaa ttggaatgc ttactacaat gagaagttca agggcaaggc cacactgact 660
gcagacaaat cctccagcac agcgtccatg gagctccgca gcctgacatc tgaggactct 720
gcggtctatt tctgtgcaag acggggatcc tacggtagta actacgactg gtacttcgat 780
gtctggggcc aagggaccac ggtcaccgtc tcctccggag gtggtggctc cgacgtccaa 840
ctggtgcagt caggggctga agtgaaaaaa cctggggcct cagtgaaggt gtcctgcaag 900
gcttctggct acacctttac taggtacacg atgcactggg taaggcaggc acctggacag 960
ggtctggaat ggattggata cattaatcct agccgtgggt atactaatta cgcagacagc 1020
gtcaagggcc gcttcacaat cactacagac aaatccacca gcacagccta catggaactg 1080
agcagcctgc gttctgagga cactgcaacc tattactgtg caagatatta tgatgatcat 1140
tactgccttg actactgggg ccaaggcacc acggtcaccg tctcctcagg cgaagggtact 1200
agtactgggt ctggtggaag tggaggttca ggtggagcag acgacattgt actgaccag 1260
tctccagcaa ctctgtctct gtctccaggg gagcgtgcca ccctgagctg cagagccagt 1320
caaagtgtaa gttacatgaa ctggtaccag cagaagccgg gcaaggcacc caaaagatgg 1380
atztatgaca catccaaagt ggcttctgga gtcctgtctc gcttcagtgg cagtgggtct 1440
gggaccgact actctctcac aatcaacagc ttggaggctg aagatgctgc cacttattac 1500
tgccaacagt ggagtagtaa cccgctcacg ttcggtggcg ggaccaaggt ggagatcaaa 1560

```

<210> 55

<211> 520

<212> PRT

<213> artificial sequence

<220>

<223> 3-5(VL-VH)xanti-CD3 (VH(5)-VL(2))

<400> 55

```

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1           5           10           15

```

```

Val His Ser Ala Arg Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu

```

Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln
50 55 60

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
65 70 75 80

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85 90 95

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
 . 100 105 110

Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr
115 120 125

Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu
145 150 155 160

Val Arg Pro Gly Thr Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr
165 170 175

Thr Phe Thr Ser Tyr Gly Leu Ser Trp Val Lys Gln Arg Thr Gly Gln
180 185 190

Gly Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile Gly Asn Ala Tyr
195 200 205

Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser
210 215 220

Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser
225 230 235 240

Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Gly Ser Asn Tyr Asp
245 250 255

Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
260 265 270

Gly Gly Gly Gly Ser Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val
275 280 285

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
290 295 300

Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly Gln
305 310 315 320

Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn
325 330 335

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser
340 345 350

Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
355 360 365

Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp
370 375 380

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr
385 390 395 400

Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile
405 410 415

Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg
420 425 430

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp
435 440 445

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr
450 455 460

Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
465 470 475 480

Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala
485 490 495

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly
 500 505 510

Gly Gly Thr Lys Val Glu Ile Lys
 515 520

<210> 56
 <211> 40
 <212> DNA
 <213> artificial sequence

<220>
 <223> Me81

<400> 56
 ggatgcgcgc gagctcgtga tgaccagac tccactctcc 40

<210> 57
 <211> 1545
 <212> DNA
 <213> artificial sequence

<220>
 <223> 4-1(VL-VH)xanti-CD3(VH(5)-VL(2)).

<400> 57
 atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt aactccgag 60
 ctctgtgatga cacagtctcc atcctccctg agtgtgtcag caggagagaa ggtcactatg 120
 agctgcaagt ccagtcagag tctgttaaac agtggaatc aaaagaacta cttggcctgg 180
 taccagcaga aaccagggca gcctcctaaa ctgttgatct acggggcatc cactagggaa 240
 tctgggggtcc ctgatcgctt cacaggcagt ggatctggaa cagatttcac tctcaccatc 300
 agcagtgtgc aggctgaaga cctggcagtt tattactgtc agaatgatta tagttatccg 360
 tacacgttcg gaggggggac caagcttgag atcaaagggtg gtggtggttc tggcggcggc 420
 ggctccggtg gtggtggttc tgaggtgcag ctgctcgagc agtctggagc tgagctggta 480
 aggcctggga cttcagtgaa gatatcctgc aaggcttctg gatacgctt cactaactac 540
 tggctagggtt gggttaagca gaggcctgga catggacttg aatgggttgg agatattttc 600
 cctggaagtg gtaatgctca ctacaatgag aagttcaagg gcaaagccac actgactgca 660
 gacaagtcct cgtacacagc ctatatgcag ctcatagacc tgacatctga ggactctgct 720
 gtctattttct gtgcaagatt gcggaactgg gacgaggcta tggactactg gggccaaggg 780
 accacggtca ccgtctcctc cggaggtggt ggctccgagc tccaactggt gcagtcaggg 840
 gctgaagtga aaaaacctgg ggcctcagtg aaggtgtcct gcaaggcttc tggctacacc 900


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tttactaggt acacgatgca ctgggtaagg caggcacctg gacagggctct ggaatggatt 960
ggatacatta atcctagccg tgggtatact aattacgcag acagcgtcaa gggccgcttc 1020
acaatcacta cagacaaatc caccagcaca gcctacatgg aactgagcag cctgcgttct 1080
gaggacactg caacctatta ctgtgcaaga tattatgatg atcattactg ccttgactac 1140
tgggggccaag gcaccacggt caccgtctcc tcaggcgaag gtactagtagc tgggtctggt 1200
ggaagtggag gttcaggtgg agcagacgac attgtactga ccagtcctcc agcaactctg 1260
tctctgtctc caggggagcg tgccaccctg agctgcagag ccagtcaaag tgtaagttac 1320
atgaactggg accagcagaa gccggggcaag gcacccaaaa gatggattta tgacacatcc 1380
aaagtggctt ctggagtccc tgctcgcttc agtggcagtg ggtctgggac cgactactct 1440
ctcacaatca acagcttgga ggctgaagat gctgccactt attactgcca acagtggagt 1500
agtaaccgcg tcacgttcgg tggcgggacc aaggtggaga tcaaa 1545

```

<210> 58

<211> 515

<212> PRT

<213> artificial sequence

<220>

<223> 4-1(VL-VH)xanti-CD3(VH(5)-VL(2))

<400> 58

```

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1           5           10           15

```

```

Val His Ser Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Ser Val
          20           25           30

```

```

Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu
          35           40           45

```

```

Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys
          50           55           60

```

```

Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Gly Ala Ser Thr Arg Glu
65           70           75           80

```

```

Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
          85           90           95

```

```

Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr

```

100	105	110
Cys Gln Asn Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys 115 120 125		
Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly 130 135 140		
Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val 145 150 155 160		
Arg Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala 165 170 175		
Phe Thr Asn Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly 180 185 190		
Leu Glu Trp Val Gly Asp Ile Phe Pro Gly Ser Gly Asn Ala His Tyr 195 200 205		
Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser 210 215 220		
Tyr Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala 225 230 235 240		
Val Tyr Phe Cys Ala Arg Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr 245 250 255		
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser 260 265 270		
Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala 275 280 285		
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr 290 295 300		
Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile 305 310 315 320		
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val 325 330 335		

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 340 345 350

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
 355 360 365

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 370 375 380

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 385 390 395 400

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 405 410 415

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 420 425 430

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 435 440 445

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 450 455 460

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 465 470 475 480

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 485 490 495

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 500 505 510

Glu Ile Lys
 515

<210> 59
 <211> 44
 <212> DNA
 <213> artificial sequence

<220>
 <223> Me92a

<400> 59
 ggattgtaca ctccgagctc gtgatgacac agtctccatc ctcc

<210> 60
<211> 1560
<212> DNA
<213> artificial sequence

<220>
<223> .4-7 (VL-VH)xanti-CD3 (VH(5)-VL(2))

<400> 60
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt acactccgcg 60
cgcgagctcg tgatgaccca gactccactc tccctgcctg tcagtcttgg agatcaagcc 120
tccatctctt gcagatctag tcagagcctt gtacacagta atggaaacac ctattttacat 180
tggtacctgc agaagccagg ccagtctcca aagctcctga tctacaaagt ttccaaccga 240
ttttctgggg tcccagacag gttcagtggc agtggatcag ggacagattt cacactcaag 300
atcagcagag tggaggctga ggatctggga gtttatttct gctctcaaag tacacatggt 360
ccgtacacgt tccgaggggg gaccaagctt gagatcaaag gtggtggtgg ttctggcggc 420
ggcggctccg gtggtggtgg ttctgaggtg cagctgctcg agcagtctgg agctgagctg 480
gcgaggcctg gggcttcagt gaagctgtcc tgcaaggctt ctggctacac cttcacaac 540
tatggtttaa gctgggtgaa gcagaggcct ggacaggctc ttgagtggat tggagagggt 600
tattctagaa ttggaatgc ttactacaat gagaagttca agggcaaggc cacactgact 660
gcagacaaat cctccagcac agcgtccatg gagctccgca gcctgacctc tgaggactct 720
gcggtctatt tctgtgcaag acggggatcc tacgatacta actacgactg gtacttcgat 780
gtctggggcc aagggaaccac ggtcaccgtc tctccggag gtggtggctc cgacgtccaa 840
ctggtgcagt caggggctga agtgaaaaaa cctggggcct cagtgaagggt gtcttgcaag 900
gcttctggct acacctttac taggtacacg atgcactggg taaggcaggc acctggacag 960
ggtctggaat ggattggata cattaatcct agccgtgggt atactaatta cgcagacagc 1020
gtcaaggggc gttcacaat cactacagac aaatccacca gcacagccta catggaactg 1080
agcagcctgc gttctgagga cactgcaacc tattactgtg caagatatta tgatgatcat 1140
tactgccttg actactgggg ccaaggcacc acggtcaccg tctcctcagg cgaagggtact 1200
agtactggtt ctggtggaag tggaggttca ggtggagcag acgacattgt actgaccag 1260
tctccagcaa ctctgtctct gtctccaggg gagcgtgcc aacctgagctg cagagccagt 1320
caaagtgtaa gttacatgaa ctggtaccag cagaagccgg gcaaggcacc caaaagatgg 1380
atztatgaca catccaaagt ggcttctgga gtccctgctc gcttcagtgg cagtgggtct 1440
gggaccgact actctctcac aatcaacagc ttggaggctg aagatgctgc cacttattac 1500

tgccaacagt ggagtagtaa cccgctcacg ttcggtggcg ggaccaaggt ggagatcaaa 1560

<210> 61

<211> 520

<212> PRT

<213> artificial sequence

<220>

<223> 4-7(VL-VH)xanti-CD3(VH(5)-VL(2))

<400> 61

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Ala Arg Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu
20 25 30

Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
35 40 45

Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln
50 55 60

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
65 70 75 80

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85 90 95

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
100 105 110

Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr
115 120 125

Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu
145 150 155 160

Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr
165 170 175

Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln Arg Pro Gly Gln

180	185	190
Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile Gly Asn Ala Tyr		
195	200	205
Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser		
210	215	220
Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser		
225	230	235
Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp Thr Asn Tyr Asp		
245	250	255
Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser		
260	265	270
Gly Gly Gly Gly Ser Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val		
275	280	285
Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr		
290	295	300
Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly Gln		
305	310	315
Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn		
325	330	335
Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser		
340	345	350
Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr		
355	360	365
Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp		
370	375	380
Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr		
385	390	395
Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile		
405	410	415

Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg
 420 425 430

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp
 435 440 445

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr
 450 455 460

Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
 465 470 475 480

Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala
 485 490 495

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly
 500 505 510

Gly Gly Thr Lys Val Glu Ile Lys
 515 520

<210> 62

<211> 1545

<212> DNA

<213> artificial sequence

<220>

<223> 5-10 (VL-VH)xanti-CD3 (VH(5)-VL(2))

<400> 62

atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt acactccgag	60
ctcgtgatga cacagtctcc atcctccctg actgtgacag caggagagaa ggtcactatg	120
agctgcaagt ccagtcagag tctgttaaac agtggaatc aaaagaacta cttgacctgg	180
taccagcaga aaccagggca gcctcctaaa ctgttgatct actgggcata cactagggaa	240
tctgggggtcc ctgatcgctt cacaggcagt ggatctggaa cagatttcac tctcaccatc	300
agcagtgtgc aggctgaaga cctggcagtt tattactgtc agaatgatta tagttatccg	360
ctcacgttcg gtgctgggac caagcttgag atcaaagggtg gtggtggttc tggcggcggc	420
ggctccggtg gtggtggttc tgagggtgcag ctgctcgagc agtctggagc tgagctggta	480
aggcctggga cttcagtgaa gatatactgc aaggcttctg gatacgctt cactaaactac	540
tggctaggtt gggtaaagca gaggcctgga catggacttg agtggattgg agatattttc	600
cctggaagtg gtaatatcca ctacaatgag aagttcaagg gcaaagccac actgactgca	660

gacaaatctt cgagcacagc ctatatgcag ctcahtagcc tgacatttga ggactctgct 720
 gtctatttct gtgcaagact gaggaactgg gacgagccta tggactactg gggccaaggg 780
 accacgggtca ccgtctcctc cggagggtgg ggctccgacg tccaactggg gcagtcaggg 840
 gctgaagtga aaaaacctgg ggctcagtg aaggtgtcct gcaaggcttc tggtacacc 900
 ttctactaggt acacgatgca ctgggtaagg caggcacctg gacagggtct ggaatggatt 960
 ggatacatta atcctagccg tggttatact aattacgcag acagcgtcaa gggccgcttc 1020
 acaatcacta cagacaaatc caccagcaca gcctacatgg aactgagcag cctgcgttct 1080
 gaggacactg caacctatta ctgtgcaaga tattatgatg atcattactg ccttgactac 1140
 tggggccaag gcaccacggg caccgtctcc tcaggcgaag gtactagtac tggttctggt 1200
 ggaagtggag gttcaggtgg agcagacgac attgtactga ccagtcctcc agcaactctg 1260
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 atgaactggg accagcagaa gccgggcaag gcacccaaaa gatggattta tgacacatcc 1380
 aaagtggctt ctggagtccc tgctcgcttc agtggcagtg ggtctgggac cgactactct 1440
 ctcaaatca acagcttgga ggctgaagat gctgccactt attactgcca acagtggagt 1500
 agtaaccgcg tcacgttcgg tggcgggacc aaggtggaga tcaaa 1545

<210> 63

<211> 515

<212> PRT

<213> artificial sequence

<220>

<223> 5-10 (VL-VH)xanti-CD3 (VH(5)-VL(2))

<400> 63

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15

Val His Ser Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val
 20 25 30

Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu
 35 40 45

Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys
 50 55 60

Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu
 65 70 75 80

Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
85 90 95

Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr
100 105 110

Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys
115 120 125

Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val
145 150 155 160

Arg Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala
165 170 175

Phe Thr Asn Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly
180 185 190

Leu Glu Trp Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr
195 200 205

Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser
210 215 220

Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala
225 230 235 240

Val Tyr Phe Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr
245 250 255

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
260 265 270

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
275 280 285

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
290 295 300

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile

305 310 315 320
 Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
 325 330 335
 Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 340 345 350
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
 355 360 365
 Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 370 375 380
 Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 385 390 395 400
 Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 405 410 415
 Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 420 425 430
 Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 435 440 445
 Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 450 455 460
 Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 465 470 475 480
 Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 485 490 495
 Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 500 505 510
 Glu Ile Lys
 515

<210> 64

<211> 1500

<212> DNA

<213> artificial sequence

<220>

<223> VH5/VL2x3-5

<400> 64

gacgtccaac	tggtgcagtc	aggggctgaa	gtgaaaaaac	ctggggcctc	agtgaaggtg	60
tcctgcaagg	cttctggcta	cacctttact	aggtacacga	tgcactgggt	aaggcaggca	120
cctggacagg	gtctggaatg	gattggatac	attaatccta	gccgtgggta	tactaattac	180
gcagacagcg	tcaagggccg	cttcacaatc	actacagaca	aatccaccag	cacagcctac	240
atggaactga	gcagcctgcg	ttctgaggac	actgcaacct	attactgtgc	aagatattat	300
gatgatcatt	actgccttga	ctactggggc	caaggcacca	cggtcacogt	ctcctcaggc	360
gaaggctacta	gtactgggtc	tggtggaagt	ggagggttcag	gtggagcaga	cgacattgta	420
ctgaccocagt	ctccagcaac	tctgtctctg	tctccagggg	agcgtgccac	cctgagctgc	480
agagccagtc	aaagtgtgaa	ttacatgaac	tggtaccagc	agaagccggg	caaggcaccc	540
aaaagatgga	tttatgacac	atccaaagtg	gcttctggag	tccctgctcg	cttcagtggc	600
agtgggtctg	ggaccgacta	ctctctcaca	atcaacagct	tggaggctga	agatgctgcc	660
acttattact	gccaacagtg	gagtagtaac	ccgctcacgt	tcgggtggcg	gaccaaggtg	720
gagatcaaat	ccggaggtgg	tggatccgag	gtgcagctgc	tcgagcagtc	tggagctgag	780
ctggtaaggc	ctgggacttc	agtgaagctg	tcctgcaagg	cttctggcta	caccttcaca	840
agctatgggt	taagctgggt	gaagcagaga	actggacagg	gccttgagtg	gattggagag	900
gtttatccta	gaattggtaa	tgcttactac	aatgagaagt	tcaagggcaa	ggccacactg	960
actgcagaca	aatcctccag	cacagcgtcc	atggagctcc	gcagcctgac	atctgaggac	1020
tctgcggtct	atttctgtgc	aagacgggga	tcctacggta	gtaactacga	ctggtacttc	1080
gatgtctggg	gccaagggac	cacggtcacc	gtctcctcag	gtgggtgggtg	ttctggcggc	1140
ggcggtccg	gtgggtgggtg	ttctgagctc	gtgatgacct	agactccact	ctccctgcct	1200
gtcagtcttg	gagatcaagc	ctccatctct	tgcagatcta	gtcagagcct	tgtacacagt	1260
aatggaaaca	cctattttaca	ttggtacctg	cagaagccag	gccagtctcc	aaagctcctg	1320
atctacaaag	tttccaaccg	attttctggg	gtcccagaca	ggttcagtgg	cagtggatca	1380
gggacagatt	tcacactcaa	gatcagcaga	gtggaggctg	aggatctggg	agttttatttc	1440
tgctctcaaa	gtacacatgt	tccgtacacg	ttcggagggg	ggaccaagct	tgagatcaaa	1500

<210> 65

<211> 500

<212> PRT

<213> artificial sequence

<220>

<223> VH5/VL2x3-5

<400> 65

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln
 245 250 255

Ser Gly Ala Glu Leu Val Arg Pro Gly Thr Ser Val Lys Leu Ser Cys
 260 265 270

Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Gly Leu Ser Trp Val Lys
 275 280 285

Gln Arg Thr Gly Gln Gly Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg
 290 295 300

Ile Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu
 305 310 315 320

Thr Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu
 325 330 335

Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr
 340 345 350

Gly Ser Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr
 355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380

Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu Pro
 385 390 395 400

Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
 405 410 415

Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys
 420 425 430

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
 435 440 445

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
 450 455 460

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe
 465 470 475 480

Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys
 485 490 495

Leu Glu Ile Lys
 500

<210> 66
 <211> 1491
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH5/VL2x4-1

<400> 66
 gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaaggtg 60
 tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120
 cctggacagg gtctggaatg gattggatac attaataccta gccgtgggta tactaattac 180
 gcagacagcg tcaagggccg cttcacaaac actacagaca aatccaccag cacagcctac 240
 atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
 gaaggctacta gtactggttc tgggtggaagt ggagggtcag gtggagcaga cgacattgta 420
 ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480
 agagccagtc aaagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
 acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg 720
 gagatcaaat ccggagggtg tggatccgag gtgcagctgc tcgagcagtc tggagctgag 780
 ctggtaaggc ctgggacttc agtgaagata tcctgcaagg cttctggata cgccttcact 840
 aactactggc taggttgggt taagcagagg cctggacatg gacttgaatg gggttgagat 900
 attttcctg gaagtggtaa tgctcactac aatgagaagt tcaagggcaa agccacactg 960
 actgcagaca agtctctgta cacagcctat atgcagctca gtagcctgac atctgaggac 1020

tctgctgtct atttctgtgc aagattgcgg aactgggacg aggctatgga ctactggggc 1080
 caagggacca cggtcaccgt ctccctcaggt ggtggtggtt ctggcggcgg cggctccggt 1140
 ggtggtggtt ctgagctcgt gatgacacag tctccatcct ccctgagtgt gtcagcagga 1200
 gagaagggtca ctatgagctg caagtccagt cagagtctgt taaacagtgg aaatcaaaag 1260
 aactacttgg cctggtacca gcagaaacca gggcagcctc ctaaactgtt gatctacggg 1320
 gcatccacta gggaatctgg ggtccctgat cgcttcacag gcagtggatc tggaacagat 1380
 ttcactctca ccatcagcag tgtgcaggct gaagacctgg cagtttatta ctgtcagaat 1440
 gattatagtt atccgtacac gttcggaggg gggaccaagc ttgagatcaa a 1491

<210> 67
 <211> 497
 <212> PRT
 <213> artificial sequence

<220>
 <223> VH5/VL2x4-1

<400> 67

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln
 245 250 255

Ser Gly Ala Glu Leu Val Arg Pro Gly Thr Ser Val Lys Ile Ser Cys
 260 265 270

Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Trp Leu Gly Trp Val Lys
 275 280 285

Gln Arg Pro Gly His Gly Leu Glu Trp Val Gly Asp Ile Phe Pro Gly
 290 295 300

Ser Gly Asn Ala His Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu
 305 310 315 320

Thr Ala Asp Lys Ser Ser Tyr Thr Ala Tyr Met Gln Leu Ser Ser Leu
 325 330 335

Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Leu Arg Asn Trp
 340 345 350

Asp Glu Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 355 360 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 370 375 380

Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Ser Val Ser Ala Gly
 385 390 395 400

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
 405 410 415

Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 420 425 430

Pro Pro Lys Leu Leu Ile Tyr Gly Ala Ser Thr Arg Glu Ser Gly Val
 435 440 445

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 450 455 460

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
 465 470 475 480

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
 485 490 495

Lys

<210> 68
 <211> 18
 <212> PRT
 <213> artificial sequence

<220>
 <223> non-deimmunized linker sequence

<400> 68

Val Glu Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
 1 5 10 15

Val Asp

<210> 69
 <211> 357
 <212> DNA

<213> artificial sequence

<220>

<223> anti-CD3 VH2

<400> 69

```

gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg      60
tcctgcaagg cttctggcta caccgctact aggtacacga tgcactgggt aaggcaggca      120
cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac      180
gcacagaagt tgcagggccg cgtcacaaatg actacagaca cttccaccag cacagcctac      240
atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat      300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctca      357

```

<210> 70

<211> 119

<212> PRT

<213> artificial sequence

<220>

<223> anti-CD3 VH2

<400> 70

```

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1          5          10          15

```

```

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ala Thr Arg Tyr
20          25          30

```

```

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35          40          45

```

```

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu
50          55          60

```

```

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65          70          75          80

```

```

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85          90          95

```

```

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100          105          110

```

```

Thr Thr Val Thr Val Ser Ser
115

```

<210> 71
 <211> 357
 <212> DNA
 <213> artificial sequence

<220>
 <223> anti-CD3 VH3

<400> 71
 gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaaggtg 60
 tcctgcaagg cttctggcta caccgctact aggtacacga tgcactgggt aaggcaggca 120
 cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 180
 gcacagaagt tgcagggccg cgtcacaatg actacagaca cttccaccag cacagcctac 240
 ctgcaaataa acagcctgaa aactgaggac actgcagtct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctca 357

<210> 72
 <211> 119
 <212> PRT
 <213> artificial sequence

<220>
 <223> anti-CD3 VH3

<400> 72

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala 15
 1 5 10
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ala Thr Arg Tyr 30
 20 25 30
 Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile 45
 35 40 45
 Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu 60
 50 55 60
 Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr 80
 65 70 75 80
 Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys 95
 85 90 95
 Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly

100

105

110

Thr Thr Val Thr Val Ser Ser
115

<210> 73

<211> 357

<212> DNA

<213> artificial sequence

<220>

<223> anti-CD3 VH5

<400> 73

gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaaggtg 60

tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120

cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 180

gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240

atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300

gatgatcatt actgccttga ctactggggc caaggcacca cggtcacctg ctctca 357

<210> 74

<211> 119

<212> PRT

<213> artificial sequence

<220>

<223> anti-CD3 VH5

<400> 74

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210>	75
<211>	357
<212>	DNA
<213>	artificial sequence

<220>
<223> anti-CD3 VH7

<400>	75								
gacgtccaac	tggtgcagtc	aggggctgaa	gtgaaaaaac	ctggggcctc	agtgaaggtg				60
tcttgcaagg	cttctggcta	cacctttact	aggtacacga	tgcactgggt	aaggcaggca				120
cctggacagg	gtctggaatg	gattggatac	attaatccta	gccgtgggta	tactaattac				180
aatcagaagt	tcaaggaccg	cgtcacaatc	actacagaca	aatccaccag	cacagcctac				240
atggaactga	gcagcctgcg	ttctgaggac	actgcagtc	attactgtgc	aagatattat				300
gatgatcatt	actgccttga	ctactggggc	caaggcacca	cggtcaccgt	ctcctca				357

```
<210> 76
<211> 119
<212> PRT
<213> artificial sequence
```

<220>
<223> anti-CD3 VH7

<400> 76

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 77
<211> 318
<212> DNA
<213> artificial sequence

<220>
<223> anti-CD3 VL1

<400> 77
gacattcaga tgaccagtc tccatctagc ctgtctgcat ctgtcgggga ccgtgtcacc 60
atcacctgca gagccagtca aagtgttaagt tacatgaact ggtaccagca gaagccgggc 120
aaggcaccga aaagatggat ttatgacaca tccaaagtgg cttctggagt ccttgcctgc 180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cgggtggcggg 300
accaaggtgg agatcaaa 318

<210> 78
<211> 106
<212> PRT
<213> artificial sequence

<220>
<223> anti-CD3 VL1

<400> 78

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 79

<211> 318

<212> DNA

<213> artificial sequence

<220>

<223> anti-CD3 VL2

<400> 79

gacattgtac tgaccagtc tccagcaact ctgtctctgt ctccagggga gcgtgccacc 60

ctgagctgca gagccagtca aagtgttaagt tacatgaact ggtaccagca gaagccgggc 120

aaggcaccga aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180

ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240

gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cgggtggcggg 300

accaaggtgg agatcaaa 318

<210> 80

<211> 106

<212> PRT

<213> artificial sequence

<220>

<223> anti-CD3 VL2

<400> 80

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
 20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr

35

40

45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 81
 <211> 318
 <212> DNA
 <213> artificial sequence

<220>
 <223> anti-CD3 VL3

<400> 81
 gacattgtac tgaccagtc tccagcaact ctgtctctgt ctccagggga gcgtgccacc 60
 ctgacctgca gagccagttc aagtgttaagt tacatgaact ggtaccagca gaagccgggc 120
 aaggcaccga aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
 ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
 gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cggtggcggg 300
 accaaggtgg agatcaaa 318

<210> 82
 <211> 106
 <212> PRT
 <213> artificial sequence

<220>
 <223> anti-CD3 VL3

<400> 82

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
 20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
 35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 83
 <211> 30
 <212> DNA
 <213> artificial sequence

<220>
 <223> vH CDR1 anti-CD3 wt

<400> 83
 ggctacacct ttactaggta cacgatgcac

30

<210> 84
 <211> 10
 <212> PRT
 <213> artificial sequence

<220>
 <223> vH CDR1 anti-CD3 wt

<400> 84

Gly Tyr Thr Phe Thr Arg Tyr Thr Met His
 1 5 10

<210> 85
 <211> 30
 <212> DNA
 <213> artificial sequence

<220>
 <223> vH CDR1 VH2,3

<400> 85
 ggctacaccg ctactaggta cacgatgcac

30

<210> 86

<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> vH CDR1 VH2,3

<400> 86

Gly Tyr Thr Ala Thr Arg Tyr Thr Met His
1 5 10

<210> 87
<211> 30
<212> DNA
<213> artificial sequence

<220>
<223> vH CDR1 VH5,7

<400> 87
ggctacacct ttactagcta cacgatgcac

30

<210> 88
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> vH CDR1 VH5,7

<400> 88

Gly Tyr Thr Phe Thr Arg Tyr Thr Met His
1 5 10

<210> 89
<211> 51
<212> DNA
<213> artificial sequence

<220>
<223> vH CDR2 wt anti-CD3 VH7

<400> 89
tacattaatc ctagccgtgg ttatactaata tacaatcaga agttcaagga c

51

<210> 90
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> vH CDR2 wt anti-CD3 VH7

<400> 90

Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys
1 5 10 15

Asp.

<210> 91

<211> 51

<212> DNA

<213> artificial sequence

<220>

<223> vH CDR2 VH5

<400> 91

tacattaatc ctagccgtgg ttataactaat tacgcagaca gcgtcaaggg c

51

<210> 92

<211> 17

<212> PRT

<213> artificial sequence

<220>

<223> vH CDR2 VH5

<400> 92

Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 93

<211> 51

<212> DNA

<213> artificial sequence

<220>

<223> vH CDR2 VH2,3

<400> 93

tacattaatc ctagccgtgg ttataactaat tacgcacaga agttgcaggg c

51

<210> 94

<211> 17

<212> PRT

<213> artificial sequence

<220>

<223> vH CDR2 VH2,3

<400> 94

Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu Gln
1 5 10 15

Gly

<210> 95

<211> 30

<212> DNA

<213> artificial sequence

<220>

<223> vH CDR3 wt anti-CD3 VH2,3,5,7

<400> 95

tattatgatg atcattactg ccttgactac

30

<210> 96

<211> 10

<212> PRT

<213> artificial sequence

<220>

<223> vH CDR3 wt anti-CD3 VH2,3,5,7

<400> 96

Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr
1 5 10

<210> 97

<211> 30

<212> DNA

<213> artificial sequence

<220>

<223> vK CDR1 wt anti-CD3 VL3

<400> 97

agagccagtt caagtgtgaag ttacatgaac

30

<210> 98

<211> 10

<212> PRT

<213> artificial sequence

<220>

<223> vK CDR1 wt anti-CD3 VL3

<400> 98

Arg Ala Ser Ser Ser Val Ser Tyr Met Asn
1 5 10

<210> 99
<211> 30
<212> DNA
<213> artificial sequence

<220>
<223> vK CDR1 VL 1,2

<400> 99
agagccagtc aaagtgtgtaag ttacatgaac

30

<210> 100
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> vK CDR1 VL 1,2

<400> 100

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn
1 5 10

<210> 101
<211> 21
<212> DNA
<213> artificial sequence

<220>
<223> vK CDR2 wt anti-CD3 VL1-3

<400> 101
gacacatcca aagtggcttc t

21

<210> 102
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> vK CDR2 wt anti-CD3 VL1-3

<400> 102

Asp Thr Ser Lys Val Ala Ser
1 5

<210> 103
<211> 27
<212> DNA

<213> artificial sequence

<220>

<223> vK CDR3 wt anti-CD3 VL1-3

<400> 103

caacagtgga gtagtaaccc gctcacg

27

<210> 104

<211> 9

<212> PRT

<213> artificial sequence

<220>

<223> vK CDR3 wt anti-CD3 VL1-3

<400> 104

Gln Gln Trp Ser Ser Asn Pro Leu Thr

1

5

<210> 105

<211> 357

<212> DNA

<213> artificial sequence

<220>

<223> vH anti-CD3 with the mutations of cys->ser

<400> 105

gatatcaaac tgcagcagtc aggggctgaa ctggcaagac ctggggcctc agtgaagatg 60

tcctgcaaga cttctggcta cacctttact aggtacacga tgcactgggt aaaacagagg 120

cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 180

aatcagaagt tcaaggacaa ggccacattg actacagaca aatcctccag cacagcctac 240

atgcaactga gcagcctgac atctgaggac tctgcagtct attactgtgc aagatattat 300

gatgatcatt actcccttga ctactggggc caaggcacca ctctcacagt ctctctca 357

<210> 106

<211> 119

<212> PRT

<213> artificial sequence

<220>

<223> vH anti-CD3 with the mutations of cys ->ser

<400> 106

Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala

1

5

10

15

Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
 50 55 60

Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Ser Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Leu Thr Val Ser Ser
 115

<210> 107

<211> 30

<212> DNA

<213> artificial sequence

<220>

<223> vH CDR3 anti-CD3 with the mutation cys-> ser

<400> 107

tattatgatg atcattaactc ccttgactac

30

<210> 108

<211> 10

<212> PRT

<213> artificial sequence

<220>

<223> vH CDR3 anti-CD3 with the mutation cys-> ser

<400> 108

Tyr Tyr Asp Asp His Tyr Ser Leu Asp Tyr
 1 5 10

<210> 109

<211> 357

<212> DNA

<213> artificial sequence

<220>

<223> wild type anti-CD3 VH

<400> 109

```

gatatcaaac tgcagcagtc aggggctgaa ctggcaagac ctggggcctc agtgaagatg      60
tcctgcaaga cttctggcta cacctttact aggtacacga tgcactgggt aaaacagagg      120
cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac      180
aatcagaagt tcaaggacaa ggccacattg actacagaca aatcctccag cacagcctac      240
atgcaactga gcagcctgac atctgaggac tctgcagtct attactgtgc aagatattat      300
gatgatcatt actgccttga ctactggggc caaggcacca ctctcacagt ctctca      357

```

<210> 110

<211> 119

<212> PRT

<213> artificial sequence

<220>

<223> wild type anti-CD3 VH

<400> 110

```

Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
1           5           10           15

```

```

Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr
          20           25           30

```

```

Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
          35           40           45

```

```

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
          50           55           60

```

```

Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr
65           70           75           80

```

```

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
          85           90           95

```

```

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
          100           105           110

```

```

Thr Thr Leu Thr Val Ser Ser
          115

```


<210> 111
 <211> 318
 <212> DNA
 <213> artificial sequence

<220>
 <223> wild type anti-CD3 VK

<400> 111
 gacattcagc tgaccagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 60
 atgacctgca gagccagttc aagtgttaagt tacatgaact ggtaccagca gaagtcaggc 120
 acctcccca aaagatggat ttatgacaca tccaaagtgg cttctggagt cccttatcgc 180
 ttcagtggca gtgggtctgg gacctcatatc tctctcacia tcagcagcat ggaggctgaa 240
 gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cggtgctggg 300
 accaagctgg agctgaaa 318

<210> 112
 <211> 106
 <212> PRT
 <213> artificial sequence

<220>
 <223> wild type anti-CD3 VK

<400> 112

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
 1 5 10 15

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
 20 25 30

Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
 35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Tyr Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
 85 90 95

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 100 105

<210> 113
 <211> 372
 <212> DNA
 <213> artificial sequence

<220>
 <223> CD19 VH

<400> 113
 caggtgcagc tgcagcagtc tggggctgag ctggtgaggc ctgggtcctc agtgaagatt 60
 tcttgcaagg cttctggcta tgcattcagt agctactgga tgaactgggt gaagcagagg 120
 cctggacagg gtcttgagtg gattggacag atttggcctg gagatggtga tactaactac 180
 aatggaaagt tcaagggtaa agccactctg actgcagacg aatcctccag cacagcctac 240
 atgcaactca gcagcctagc atctgaggac tctgcggtct atttctgtgc aagacgggag 300
 actacgacgg tagggcggtta ttactatgct atggactact ggggcccaagg gaccacggtc 360
 accgtctcct cc 372

<210> 114
 <211> 124
 <212> PRT
 <213> artificial sequence

<220>
 <223> CD19 VH

<400> 114

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
 1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
 20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
 65 70 75 80

Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95

Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
 100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 115
 <211> 333
 <212> DNA
 <213> artificial sequence

<220>
 <223> CD19 VL

<400> 115
 gatatccagc tgaccagtc tccagcttct ttggctgtgt ctctagggca gagggccacc 60
 atctcctgca aggccagcca aagtgttgat tatgatggtg atagttattt gaactggtac 120
 caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 180
 gggatcccac ccagggttag tggcagtggtg tctgggacag acttcaccct caacatccat 240
 cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg 300
 acgttcggtg gagggaccaa gctcgagatc aaa 333

<210> 116
 <211> 111
 <212> PRT
 <213> artificial sequence

<220>
 <223> CD19 VL

<400> 116

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
 20 25 30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
 35 40 45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 117
<211> 47
<212> DNA
<213> artificial sequence

<220>
<223> 4-7 VL BspEI FOR

<400> 117
ctgaaatccg gaggtggtgg atccgagctc gtgatgaccc agactcc

47

<210> 118
<211> 52
<212> DNA
<213> artificial sequence

<220>
<223> 4-7 VL GS15 REV

<400> 118
ggagcgcgcg ccgccagaac caccaccacc ttgatctca agcttggtcc cc

52

<210> 119
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDRH3 M1 mutant

<400> 119

His Tyr Asp Asp His Tyr Cys Leu Asp Tyr
1 5 10

<210> 120
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDRH3 M4 mutant

<400> 120

Tyr Ser Asp Asp His Tyr Cys Leu Asp Tyr
1 5 10

<210> 121
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDRH3 M7 mutant

<400> 121

Tyr Tyr Asp Ala His Tyr Cys Leu Asp Tyr
1 5 10

<210> 122
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDRH3 M9 mutant

<400> 122

Tyr Tyr Asp Asp Gln Tyr Cys Leu Asp Tyr
1 5 10

<210> 123
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDRH3 M10 mutant

<400> 123

Tyr Tyr Asp Asp Pro Tyr Cys Leu Asp Tyr
1 5 10

<210> 124
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDRH3 M11 mutant

<400> 124

Tyr Phe Asn Asp His Tyr Cys Leu Asp Tyr
1 5 10

<210> 125

<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDRH3 M13 mutant

<400> 125

Tyr Tyr Asn Asp Gln Tyr Cys Leu Asp Tyr
1 5 10

<210> 126
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDRH3 M20 mutant

<400> 126

Tyr His Asp Asp Pro Tyr Cys Leu Asp Tyr
1 5 10

<210> 127
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> CDRH3 M76 mutant

<400> 127

Tyr Tyr Asp Asp Asn Tyr Cys Leu Asp Tyr
1 5 10

<210> 128
<211> 354
<212> DNA
<213> artificial sequence

<220>
<223> CCR5 Heavy chain

<400> 128
cagctggagc agtctggacc tgaactgaag aagcctggag agacagtcac gatctcctgc 60
aaggcttctg ggtatacctt cacgaagttc ggaatgaact gggatgaagca ggctccagga 120
aagggttttaa agtggatggg ctggatacac acctccactg gagagccaac atattctgat 180
gacttcaagg gacggtttgc cttctctttg gaaacgtctg ccagcactgc ctatttgcg 240
atcaacaacc tcaaaaatga ggacatggct aaatacttct gtgccagagg tggctccttac 300

gtaaggggtg ctttggacta ctgggggtcaa ggaacctcag tcaccgtctc ctcc 354

<210> 129
<211> 118
<212> PRT
<213> artificial sequence

<220>
<223> CCR5 Heavy chain

<400> 129

Gln Leu Glu Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr Val
1 5 10 15

Thr Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Lys Phe Gly Met
20 25 30

Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met Gly Trp
35 40 45

Ile His Thr Ser Thr Gly Glu Pro Thr Tyr Ser Asp Asp Phe Lys Gly
50 55 60

Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr Leu Arg
65 70 75 80

Ile Asn Asn Leu Lys Asn Glu Asp Met Ala Lys Tyr Phe Cys Ala Arg
85 90 95

Gly Gly Pro Tyr Val Arg Gly Ala Leu Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Ser Val Thr Val Ser Ser
115

<210> 130
<211> 333
<212> DNA
<213> artificial sequence

<220>
<223> CCR5 Light chain

<400> 130

gacattatcc tgatccaatc tccaccttct ttggctgtgt ctctagggca gagggccacc 60

atctcctgca gaaccagcga aaatgttgac ggatacggca ttagttttat aaactggtac 120

```

caacagaagc caggacagcc acccaaactc ctcatctatg ctgcatccca ccaaggatcc      180
ggggtccttg ccagatttag tggcagtggg tctgggacag acttcagcct caacatccat      240
cctttggagg aggatgatac tgcaatgtat ttctgtcacc aaagtaagaa gggtccgtgg      300
acgttcggtg gaggcaccaa gctggaaatc aaa                                  333

```

```

<210> 131
<211> 111
<212> PRT
<213> artificial sequence

```

```

<220>
<223> CCR5 Light chain

```

```

<400> 131

```

```

Asp Ile Ile Leu Ile Gln Ser Pro Pro Ser Leu Ala Val Ser Leu Gly
1           5           10           15

```

```

Gln Arg Ala Thr Ile Ser Cys Arg Thr Ser Glu Asn Val Asp Gly Tyr
          20           25           30

```

```

Gly Ile Ser Phe Ile Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
          35           40           45

```

```

Lys Leu Leu Ile Tyr Ala Ala Ser His Gln Gly Ser Gly Val Pro Ala
          50           55           60

```

```

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His
65           70           75           80

```

```

Pro Leu Glu Glu Asp Asp Thr Ala Met Tyr Phe Cys His Gln Ser Lys
          85           90           95

```

```

Lys Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
          100           105           110

```

```

<210> 132
<211> 360
<212> DNA
<213> artificial sequence

```

```

<220>
<223> EpCAM5-10 heavy chain

```

```

<400> 132

```

```

gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggctggggac ttcagtgaag      60
atatcctgca aggcttctgg atacgccttc actaactact ggctaggttg ggtaaagcag      120

```


aggcctggac atggacttga gtggattgga gatattttcc ctggaagtgg taatatccac 180
 tacaatgaga agttcaaggg caaagccaca ctgactgcag acaaattctc gagcacagcc 240
 tatatgcagc tcagtagcct gacatttgag gactctgctg tctatttctg tgcaagactg 300
 aggaactggg acgagcctat ggactactgg ggccaagggg ccacggtcac cgtctcctca 360

<210> 133
 <211> 120
 <212> PRT
 <213> artificial sequence

<220>
 <223> EpCAM5-10 heavy chain

<400> 133

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
 1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
 20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
 35 40 45

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
 50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
 65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
 85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 134
 <211> 339
 <212> DNA
 <213> artificial sequence

<220>
 <223> EpCAM5-10 light chain

<400> 134
gagctcgtga tgacacagtc tccatcctcc ctgactgtga cagcaggaga gaaggtcact 60
atgagctgca agtccagtca gagtctgtta aacagtggaa atcaaaagaa ctacttgacc 120
tggtaccagc agaaaccagg gcagcctcct aaactgttga tctactgggc atccactagg 180
gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc 240
atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300
ccgctcacgt tccgtgctgg gaccaagctt gagatcaaa 339

<210> 135
<211> 113
<212> PRT
<213> artificial sequence

<220>
<223> EpCAM 5-10 light chain

<400> 135

Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
100 105 110

Lys

<210> 136
<211> 360

<212> DNA
 <213> artificial sequence

<220>

<223> EpCAM 3-1 VH

<400> 136

```

gaggtgcagc tgctcgagca gtctggagct gagctggtga aacctggggc ctcaagtgaag   60
atatcctgca aggcttctgg atacgccttc actaactact ggctaggttg ggtaaagcag   120
aggcctggac atggacttga gtggattgga gatcttttcc ctggaagtgg taatactcac   180
tacaatgaga ggttcagggg caaagccaca ctgactgcag acaaatcctc gagcacagcc   240
tttatgcagc tcagtagcct gacatctgag gactctgctg tctatttctg tgcaagattg   300
aggaactggg acgaggctat ggactactgg ggccaaggga ccacggtcac cgtctcctca   360
  
```

<210> 137

<211> 120

<212> PRT

<213> artificial sequence

<220>

<223> EpCAM 3-1 VH

<400> 137

```

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Lys Pro Gly
1           5           10           15
  
```

```

Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20           25           30
  
```

```

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35           40           45
  
```

```

Ile Gly Asp Leu Phe Pro Gly Ser Gly Asn Thr His Tyr Asn Glu Arg
50           55           60
  
```

```

Phe Arg Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65           70           75           80
  
```

```

Phe Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
85           90           95
  
```

```

Cys Ala Arg Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln
100          105          110
  
```

```

Gly Thr Thr Val Thr Val Ser Ser
  
```

115

120

<210> 138
 <211> 321
 <212> DNA
 <213> artificial sequence

<220>

<223> EpCAM 3-1 VL

<400> 138

```

gagctcggtca tgaccagtc tccatcttat cttgctgcat ctctggaga aaccattact      60
attaattgca gggcaagtaa gagcattagc aaatatttag cctggatatca agagaaacct      120
gggaaaaacta ataagcttct tatctactct ggatccactt tgcaatctgg aattccatca      180
agggttcagtg gcagtggatc tggtagacat ttcaactctca ccatcagtag cctggagcct      240
gaagattttg caatgtatta ctgtcaacag cataatgaat atccgtacac gttcggaggg      300
gggaccaagc ttgagatcaa a                                          321
  
```

<210> 139
 <211> 107
 <212> PRT
 <213> artificial sequence

<220>

<223> EpCAM 3-1 VL

<400> 139

```

Glu Leu Val Met Thr Gln Ser Pro Ser Tyr Leu Ala Ala Ser Pro Gly
1           5           10           15
  
```

```

Glu Thr Ile Thr Ile Asn Cys Arg Ala Ser Lys Ser Ile Ser Lys Tyr
20           25           30
  
```

```

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Thr Asn Lys Leu Leu Ile
35           40           45
  
```

```

Tyr Ser Gly Ser Thr Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
50           55           60
  
```

```

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65           70           75           80
  
```

```

Glu Asp Phe Ala Met Tyr Tyr Cys Gln Gln His Asn Glu Tyr Pro Tyr
85           90           95
  
```

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 140
 <211> 372
 <212> DNA
 <213> artificial sequence

<220>
 <223> EpCAM 3-5 VH

<400> 140
 gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggcttgggac ttcagtgaag 60
 ctgtcctgca aggcttctgg ctacaccttc acaagctatg gtttaagctg ggtgaagcag 120
 agaactggac agggccttga gtggattgga gaggtttatc ctagaattgg taatgcttac 180
 tacaatgaga agttcaaggg caaggccaca ctgactgcag acaaatectc cagcacagcg 240
 tccatggagc tccgcagcct gacatctgag gactctgcgg tctatttctg tgcaagacgg 300
 ggatcctacg gtagtaacta cgactgggtac ttcgatgtct ggggccaagg gaccacggtc 360
 accgtctcct ca 372

<210> 141
 <211> 124
 <212> PRT
 <213> artificial sequence

<220>
 <223> EpCAM 3-5 VH

<400> 141

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
 1 5 10 15

Thr Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser
 20 25 30

Tyr Gly Leu Ser Trp Val Lys Gln Arg Thr Gly Gln Gly Leu Glu Trp
 35 40 45

Ile Gly Glu Val Tyr Pro Arg Ile Gly Asn Ala Tyr Tyr Asn Glu Lys
 50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
 65 70 75 80

Ser Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe

85

90

95

Cys Ala Arg Arg Gly Ser Tyr Gly Ser Asn Tyr Asp Trp Tyr Phe Asp
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 142
 <211> 336
 <212> DNA
 <213> artificial sequence

<220>
 <223> EpCAM 3-5 VL

<400> 142
 gagctcgtga tgaccagac tccactctcc ctgcctgtca gtcttgaga tcaagcctcc 60
 atctcttgca gatctagtca gagccttgta cacagtaatg gaaacaccta ttacattgg 120
 tacctgcaga agccaggcca gtctccaaag ctctgatct acaaagtttc caaccgattt 180
 tctgggggtcc cagacagggtt cagtggcagt ggatcaggga cagatttcac actcaagatc 240
 agcagagtgg aggctgagga tctgggagtt tatttctgct ctcaaagtac acatgttccg 300
 tacacgttcg gaggggggac caagcttgag atcaaa 336

<210> 143
 <211> 112
 <212> PRT
 <213> artificial sequence

<220>
 <223> EpCAM 3-5 VL

<400> 143

Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
 1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
 20 25 30

Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
 85 90 95

Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 144
 <211> 360
 <212> DNA
 <213> artificial sequence

<220>
 <223> EpCAM 4-1 VH

<400> 144
 gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggcctgggaccttcagtgaag 60
 atatcctgca aggccttctgg atacgccttc actaaactact ggctagggttg ggttaagcag 120
 aggcctggac atggacttga atggggttga gatattttcc ctggaagtgg taatgctcac 180
 tacaatgaga agttcaaggg caaagccaca ctgactgcag acaagtcttc gtacacagcc 240
 tatatgcagc tcagtagcct gacatctgag gactctgctg tctatttctg tgcaagattg 300
 cggaactggg acgaggctat ggactactgg ggccaaggga ccacggtcac cgtctcctca 360

<210> 145
 <211> 120
 <212> PRT
 <213> artificial sequence

<220>
 <223> EpCAM 4-1 VH

<400> 145

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
 1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
 20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
 35 40 45

Val Gly Asp Ile Phe Pro Gly Ser Gly Asn Ala His Tyr Asn Glu Lys
 50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Tyr Thr Ala
65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 146

<211> 339

<212> DNA

<213> artificial sequence

<220>

<223> EpCAM 4-1 VL

<400> 146

gagctcgtga tgacacagtc tccatcctcc ctgagtgtgt cagcaggaga gaaggtcact 60

atgagctgca agtccagtca gagtctgtta aacagtggaa atcaaaagaa ctacttgccc 120

tggtaccagc agaaaccagg gcagcctcct aaactgttga tctacggggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300

ccgtacacgt tcggaggggg gaccaagctt gagatcaaa 339

<210> 147

<211> 113

<212> PRT

<213> artificial sequence

<220>

<223> EpCAM 4-1 VL

<400> 147

Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Ser Val Ser Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Gly Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
100 105 110

Lys

<210> 148
<211> 372
<212> DNA
<213> artificial sequence

<220>
<223> EpCAM 4-7 VH

<400> 148
gagggtgcagc tgctcgagca gtctggagct gagctggcga ggcctggggc ttcagtgaag 60
ctgtcctgca aggcttctgg ctacaccttc acaaactatg gtttaagctg ggtgaagcag 120
aggcctggac aggtccttga gtggattgga gaggtttatc ctagaattgg taatgcttac 180
tacaatgaga agttcaaggg caaggccaca ctgactgcag acaaatcctc cagcacagcg 240
tccatggagc tccgcagcct gacctctgag gactctgcgg tctatttctg tgcaagacgg 300
ggatcctacg atactaacta cgactggtac ttcgatgtct ggggccaagg gaccacggtc 360
accgtctcct ca 372

<210> 149
<211> 124
<212> PRT
<213> artificial sequence

<220>
<223> EpCAM 4-7 VH

<400> 149

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly
1 5 10 15

Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn
 20 25 30

Tyr Gly Leu Ser Trp Val Lys Gln Arg Pro Gly Gln Val Leu Glu Trp
 35 40 45

Ile Gly Glu Val Tyr Pro Arg Ile Gly Asn Ala Tyr Tyr Asn Glu Lys
 50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
 65 70 75 80

Ser Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
 85 90 95

Cys Ala Arg Arg Gly Ser Tyr Asp Thr Asn Tyr Asp Trp Tyr Phe Asp
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 150
 <211> 336
 <212> DNA
 <213> artificial sequence

<220>
 <223> EpCAM 4-7 VL

<400> 150
 gagctcgtga tgaccagac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60
 atctcttgca gatctagtca gagccttgta cacagtaatg gaaacaccta ttacattgg 120
 tacctgcaga agccaggcca gtctccaaag ctctgatct acaaagtttc caaccgattt 180
 tctgggggtcc cagacagggt cagtggcagt ggatcaggga cagatttcac actcaagatc 240
 agcagagtgg aggctgagga tctgggagtt tatttctgct ctcaaagtac acatgttccg 300
 tacacgttcg gaggggggac caagcttgag atcaaa 336

<210> 151
 <211> 112
 <212> PRT
 <213> artificial sequence

<220>
 <223> EpCAM 4-7 VL

<400> 151

Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
85 90 95

Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 152

<211> 25

<212> PRT

<213> artificial sequence

<220>

<223> VH5 Framework 1

<400> 152

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

<210> 153

<211> 25

<212> PRT

<213> artificial sequence

<220>

<223> VH7 Framework 1

<400> 153

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

<210> 154
<211> 25
<212> PRT
<213> artificial sequence

<220>
<223> VH2 Framework 1

<400> 154

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

<210> 155
<211> 25
<212> PRT
<213> artificial sequence

<220>
<223> VH3 Framework 1

<400> 155

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

<210> 156
<211> 15
<212> PRT
<213> artificial sequence

<220>
<223> VH5 Framework 2

<400> 156

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
1 5 10 15

<210> 157
<211> 15

<212> PRT
<213> artificial sequence

<220>
<223> VH7 Framework 2

<400> 157

Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Tyr
1			5						10					15

<210> 158
<211> 22
<212> PRT
<213> artificial sequence

<220>
<223> VH2 Framework 2

<400> 158

Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile
1			5						10					15	

Asn Pro Ser Arg Gly Tyr
20

<210> 159
<211> 22
<212> PRT
<213> artificial sequence

<220>
<223> VH3 Framework 2

<400> 159

Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile
1			5						10					15	

Asn Pro Ser Arg Gly Tyr
20

<210> 160
<211> 32
<212> PRT
<213> artificial sequence

<220>
<223> VH5 Framework 3

<400> 160

Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu

1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg
20 25 30

<210> 161
<211> 32
<212> PRT
<213> artificial sequence

<220>
<223> VH7 Framework 3

<400> 161

Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 162
<211> 32
<212> PRT
<213> artificial sequence

<220>
<223> VH2 Framework 3

<400> 162

Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg
20 25 30

<210> 163
<211> 32
<212> PRT
<213> artificial sequence

<220>
<223> VH3 Framework 3

<400> 163

Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 164
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> VH5 Framework 4

<400> 164

Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser
1				5					10	

<210> 165
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> VH7 Framework 4

<400> 165

Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser
1				5					10	

<210> 166
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> VH2 Framework 4

<400> 166

Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser
1				5					10	

<210> 167
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> VH3 Framework 4

<400> 167

Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser
1				5					10	

<210> 168

<211> 15
 <212> PRT
 <213> artificial sequence

<220>
 <223> Standard linker

<400> 168

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10 15

<210> 169
 <211> 366
 <212> DNA
 <213> artificial sequence

<220>
 <223> CD20VH

<400> 169
 cagggtgcaac tgcggcagcc tggggctgag ctggtgaagc ctggggcctc agtgaagatg 60
 tcctgcaagg cttctggcta cacatttacc agttacaata tgcactgggt aaagcagaca 120
 cctggacagg gcctggaatg gattggagct atttatccag gaaatggtga tacttcctac 180
 aatcagaagt tcaaaggcaa ggccacattg actgcagaca aatcctccag cacagcctac 240
 atgcagctca gcagtctgac atctgaggac tctgcggtct attactgtgc aagatcgcac 300
 tacggtagta actacgtaga ctactttgac tactggggcc aaggcacact agtcacagtc 360
 tcgaca 366

<210> 170
 <211> 122
 <212> PRT
 <213> artificial sequence

<220>
 <223> CD20VH

<400> 170

Gln Val Gln Leu Arg Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30

Asn Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Ser His Tyr Gly Ser Asn Tyr Val Asp Tyr Phe Asp Tyr Trp
 100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Thr
 115 120

<210> 171
 <211> 318
 <212> DNA
 <213> artificial sequence

<220>
 <223> CD20VL

<400> 171
 caaattgttc tctcccagtc tccagcaatc ctttctgcat ctccagggga gaaggtcaca 60
 atgacttgca gggccagctc aagtttaagt ttcattgact ggtaccagca gaagccagga 120
 tcctcccca aaccctggat ttatgccaca tccaacctgg cttctggagt cctgctcgc 180
 ttcagtggca gtgggtctgg gacctcttac tctctcacia tcagcagagt ggaggctgaa 240
 gatgctgcca cttatttctg ccatcagtgg agtagtaacc cgctcacgtt cgggtgctggg 300
 acaaaggtgg aaataaaa 318

<210> 172
 <211> 106
 <212> PRT
 <213> artificial sequence

<220>
 <223> CD20VL

<400> 172

Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
 1 5 10 15

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Leu Ser Phe Met
 20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
35 40 45

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Phe Cys His Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Ala Gly Thr Lys Val Glu Ile Lys
100 105

<210> 173
<211> 15
<212> DNA
<213> artificial sequence

<220>
<223> GGGGS linker

<400> 173
ggaggtggtg gatcc

15

<210> 174
<211> 5
<212> PRT
<213> artificial sequence

<220>
<223> GGGGS linker

<400> 174

Gly Gly Gly Gly Ser
1 5

<210> 175
<211> 18
<212> DNA
<213> artificial sequence

<220>
<223> SGGGS linker

<400> 175
tccggaggtg gtggatcc

18

<210> 176
 <211> 6
 <212> PRT
 <213> artificial sequence

<220>
 <223> SGGGGS linker

<400> 176

Ser Gly Gly Gly Gly Ser
 1 5

<210> 177
 <211> 1527
 <212> DNA
 <213> artificial sequence

<220>
 <223> antiCD19xantiCD3 VH2VL1

<400> 177

gatatccagc tgacccagtc tccagcttct ttggctgtgt ctctagggca gagggccacc	60
atctcctgca aggccagcca aagtgttgat tatgatggtg atagttattt gaactggtac	120
caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct	180
gggatcccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat	240
cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg	300
acgttcggtg gagggaccaa gctcgagatc aaagggtggtg gtggttctgg cggcggcggc	360
tccggtggtg gtggttctca ggtgcagctg cagcagctctg gggctgagct ggtgaggcct	420
gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg	480
aactgggtga agcagaggcc tggacagggt cttgagtgga ttggaagat ttggcctgga	540
gatggtgata ctaactacaa tggaaagtgc aagggttaaag cactctgac tgcagacgaa	600
tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat	660
ttctgtgcaa gacgggagac tacgacggta ggccgttatt actatgctat ggactactgg	720
ggccaaggga ccacggtcac cgtctcctcc ggagggtggtg gctccgacgt ccaactggtg	780
cagtcagggg ctgaagtga aaaacctggg gcctcagtga aggtgtcctg caaggcttct	840
ggctacaccg ctactaggtg cacgatgcac tgggtaaggc aggcacctgg acagggtctg	900
gaatggattg gatacattaa tcctagccgt gggtatacta attacgcaca gaagttgcag	960
ggccgcgtca caatgactac agacacttcc accagcacag cctacatgga actgagcagc	1020
ctgcgttctg aggacactgc aacctattac tgtgcaagat attatgatga tcattactgc	1080

cttgactact ggggccaagg caccacgggc accgtctcct caggcgaagg tactagtact 1140
 ggttctggtg gaagtggagg ttcaggtgga gcagacgaca ttcagatgac ccagtctcca 1200
 tctagcctgt ctgcatctgt cggggaccgt gtcacatca cctgcagagc cagtcaaagt 1260
 gtaagttaca tgaactggta ccagcagaag ccgggcaagg caccctaaaag atggatttat 1320
 gacacatcca aagtggcttc tggagtcctt gtcgcttca gtggcagtgg gtctgggacc 1380
 gactactctc tcacaatcaa cagcttggag gctgaagatg ctgccactta ttactgcca 1440
 cagtggagta gtaaccgct cacgttcggt ggcgggacca aggtggagat caaacatcat 1500
 caccatcatc attagagatc tgtcgac 1527

<210> 178

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> antiCD19xantiCD3 VH2VL1

<400> 178

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
 20 25 30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
 35 40 45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
 85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
 115 120 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
 130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
 145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
 165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
 180 185 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
 195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
 210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
 225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
 245 250 255

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
 260 265 270

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ala Thr Arg Tyr Thr
 275 280 285

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
 290 295 300

Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu Gln
 305 310 315 320

Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr Met
 325 330 335

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
 340 345 350

Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr
 355 360 365

Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly
 370 375 380

Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser Pro
 385 390 395 400

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
 405 410 415

Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
 420 425 430

Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly
 435 440 445

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
 450 455 460

Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
 465 470 475 480

Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
 485 490 495

Ile Lys

<210> 179
 <211> 1527
 <212> DNA
 <213> artificial sequence

<220>
 <223> antiCD19xantiCD3 VH2VL2

<400> 179
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 atctcctgca aggccagcca aagtgttgat tatgatggtg atagttatth gaactggtac 120
 caacagattc caggacagcc acccaaactc ctcatttatg atgcatccaa tctagtttct 180
 gggatccac ccagggttag tggcagtggg tctgggacag acttcaccct caacatccat 240
 cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtg 300
 acgttcggtg gagggaccaa gctcgagatc aaaggtggtg gtggttctgg cggcggcggc 360
 tccggtggtg gtggttctca ggtgcagctg cagcagctctg gggctgagct ggtgaggcct 420

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gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg 480
aactgggtga agcagaggcc tggacagggt cttgagtgga ttggacagat ttggcctgga 540
gatggtgata ctaactacaa tggaaagttc aagggtaaag ccactctgac tgcagacgaa 600
tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat 660
ttctgtgcaa gacgggagac tacgacggtg ggccgttatt actatgctat ggactactgg 720
ggccaaggga ccacggtcac cgtctcctcc ggagggtgtg gctccgacgt ccaactggtg 780
cagtcagggg ctgaagtga aaaacctggg gcctcagtga aggtgtcctg caaggcttct 840
ggctacaccg ctactaggta cacgatgcac tgggtaaggc aggcacctgg acagggtctg 900
gaatggattg gatacattaa tcctagccgt gggtatacta attacgcaca gaagttgcag 960
ggccgctca caatgactac agacacttcc accagcacag cctacatgga actgagcagc 1020
ctgcgttctg aggacactgc aacctattac tgtgcaagat attatgatga tcattactgc 1080
cttgactact ggggccaagg caccacggtc accgtctcct caggcgaagg tactagtact 1140
ggttctggtg gaagtggagg ttcagggtgga gcagacgaca ttgtactgac ccagtctcca 1200
gcaactctgt ctctgtctcc aggggagcgt gccaccctga gctgcagagc cagtcaaagt 1260
gtaagttaca tgaactggta ccagcagaag ccgggcaagg caccctaaaag atggatttat 1320
gacacatcca aagtggcttc tggagtccct gctcgcttca gtggcagtgg gtctgggacc 1380
gactactctc tcacaatcaa cagcttgag gctgaagatg ctgccactta ttactgocaa 1440
cagtggagta gtaaccgct cacgttcggt ggcgggacca aggtggagat caaacatcat 1500
caccatcatc attagagatc tgtcgac 1527

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<210> 180

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> antiCD19xantiCD3 VH2VL2

<400> 180

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Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1           5           10           15

```

```

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20           25           30

```

```

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro

```

35

40

45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
 85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
 115 120 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
 130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
 145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
 165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
 180 185 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
 195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
 210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
 225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
 245 250 255

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
 260 265 270

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ala Thr Arg Tyr Thr
 275 280 285

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
 290 295 300

Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu Gln
 305 310 315 320

Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr Met
 325 330 335

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
 340 345 350

Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr
 355 360 365

Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly
 370 375 380

Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro
 385 390 395 400

Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
 405 410 415

Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
 420 425 430

Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly
 435 440 445

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
 450 455 460

Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
 465 470 475 480

Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
 485 490 495

Ile Lys

<210> 181
 <211> 1527
 <212> DNA
 <213> artificial sequence

<220>

<223> antiCD19xantiCD3 VH2VL3

<400> 181

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atctcctgca aggccagcca aagtgttgat tatgatggtg atagttattt gaactggtac	120
caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct	180
gggatcccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat	240
cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg	300
acgttcggtg gagggaccaa gctcgagatc aaaggtggtg gtggttctgg cggcggcggc	360
tccggtggtg gtggttctca ggtgcagctg cagcagtctg gggctgagct ggtgaggcct	420
gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg	480
aactgggtga agcagaggcc tggacagggt cttgagtgga ttggacagat ttggcctgga	540
gatggtgata ctaactacaa tggaaagttc aagggttaaag ccactctgac tgcagacgaa	600
tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat	660
ttctgtgcaa gacgggagac tacgacggta ggccgttatt actatgctat ggactactgg	720
ggccaaggga ccacggtcac cgtctcctcc ggaggtggtg gctccgacgt ccaactggtg	780
cagtcagggg ctgaagtga aaaacctggg gcctcagtga aggtgtcctg caaggcttct	840
ggctacaccg ctactaggtg cacgatgcac tgggtaaggc aggcacctgg acagggtctg	900
gaatggattg gatacatcaa tcctagccgt gggtatacta attacgcaca gaagttgcag	960
ggccgcgtca caatgactac agacacttcc accagcacag cctacatgga actgagcagc	1020
ctgcgttctg aggacactgc aacctattac tgtgcaagat attatgatga tcattactgc	1080
cttgactact ggggccaaagg caccacggtc accgtctcct caggcgaagg tactagtact	1140
ggttctggtg gaagtggagg ttcagggtgga gcagacgaca ttgtactgac ccagtctcca	1200
gcaactctgt ctctgtctcc aggggagcgt gccaccctga cctgcagagc cagttcaagt	1260
gtaagttaca tgaactggta ccagcagaag ccgggcaagg cacccaaaag atggatttat	1320
gacacatcca aagtggcttc tggagtcctt gctcgcttca gtggcagtgg gtctgggacc	1380
gactactctc tcacaatcaa cagcttggag gctgaagatg ctgccactta ttactgccaa	1440
cagtggagta gtaaccgct cacgttcggt ggcgggacca aggtggagat caaacatcat	1500

caccatcatc attagagatc tgtcgac

1527

<210> 182

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> antiCD19xantiCD3 VH2VL3

<400> 182

Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ala	Val	Ser	Leu	Gly
1				5					10					15	

Gln	Arg	Ala	Thr	Ile	Ser	Cys	Lys	Ala	Ser	Gln	Ser	Val	Asp	Tyr	Asp
			20					25					30		

Gly	Asp	Ser	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Ile	Pro	Gly	Gln	Pro	Pro
	35						40					45			

Lys	Leu	Leu	Ile	Tyr	Asp	Ala	Ser	Asn	Leu	Val	Ser	Gly	Ile	Pro	Pro
50						55					60				

Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Asn	Ile	His
65				70						75					80

Pro	Val	Glu	Lys	Val	Asp	Ala	Ala	Thr	Tyr	His	Cys	Gln	Gln	Ser	Thr
			85						90					95	

Glu	Asp	Pro	Trp	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Gly
		100						105					110		

Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gln	Val
	115						120					125			

Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ser	Ser	Val
130						135					140				

Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ala	Phe	Ser	Ser	Tyr	Trp	Met
145					150					155					160

Asn	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Gln
			165						170					175	

Ile	Trp	Pro	Gly	Asp	Gly	Asp	Thr	Asn	Tyr	Asn	Gly	Lys	Phe	Lys	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys Arg
405 410 415

Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
 420 425 430

Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly
 435 440 445

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
 450 455 460

Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
 465 470 475 480

Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
 485 490 495

Ile Lys

<210> 183
 <211> 1527
 <212> DNA
 <213> artificial sequence

<220>
 <223> antiCD19xantiCD3 VH3VL1

<400> 183
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 atctctctgca aggccagcca aagtgttgat tatgatggtg atagttattt gaactggtac 120
 caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 180
 gggatcccac ccaggtttag tggcagtggg tctgggacag acttcacct caacatccat 240
 cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg 300
 acgttcggtg gagggaccaa gctcgagatc aaaggtggtg gtggttctgg cggcggcggc 360
 tccggtggtg gtggttctca ggtgcagctg cagcagtctg gggctgagct ggtgaggcct 420
 gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg 480
 aactgggtga agcagaggcc tggacagggt cttgagtgga ttggacagat ttggcctgga 540
 gatggtgata ctaactacaa tggaaagttc aagggtaaag ccactctgac tgcagacgaa 600
 tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat 660
 ttctgtgcaa gacgggagac tacgacggta ggccgttatt actatgctat ggactactgg 720
 ggccaaggga ccacggtcac cgtctcctcc ggaggtggtg gctccgacgt ccaactggtg 780

```

cagtcagggg ctgaagtgaa aaaacctggg gcctcagtga aggtgtcctg caaggcttct      840
ggctacaccg ctactaggtta cacgatgcac tgggtaaggc aggcacctgg acaggggtctg      900
gaatggattg gatacattaa tcctagccgt ggttatacta attacgcaca gaagttgcag      960
ggccgcgtca caatgactac agacacttcc accagcacag cctacctgca aatgaacagc     1020
ctgaaaactg aggacactgc agtctattac tgtgcaagat attatgatga tcattactgc     1080
cttgactact ggggccaagg caccacggtc accgtctcct caggcgaagg tactagtact     1140
ggttctggtg gaagtggagg ttcaggtgga gcagacgaca ttcagatgac ccagtctcca     1200
tctagcctgt ctgcatctgt cggggaccgt gtcacatca cctgcagagc cagtcaaagt     1260
gtaagttaca tgaaactggta ccagcagaag ccgggcaagg cacccaaaag atggatttat     1320
gacacatcca aagtggcttc tggagtcctt gctcgcttca gtggcagtgg gtctgggacc     1380
gactactctc tcacaatcaa cagcttggag gctgaagatg ctgccactta ttactgccaa     1440
cagtggagta gtaaccgct caggttcggt ggcgggacca agtggagat caaacatcat     1500
caccatcatc attagagatc tgtcgac                                     1527

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```

<210> 184
<211> 498
<212> PRT
<213> artificial sequence

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<220>
<223> antiCD19xantiCD3 VH3VL1

```

```

<400> 184

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```

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1           5           10           15

```

```

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
          20           25           30

```

```

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
35           40           45

```

```

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
50           55           60

```

```

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65           70           75           80

```

```

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
          85           90           95

```

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
 115 120 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
 130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
 145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
 165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
 180 185 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
 195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
 210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
 225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
 245 250 255

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
 260 265 270

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ala Thr Arg Tyr Thr
 275 280 285

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
 290 295 300

Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu Gln
 305 310 315 320

Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr Leu

325

330

335

Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 340 345 350

Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr
 355 360 365

Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly
 370 375 380

Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser Pro
 385 390 395 400

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
 405 410 415

Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
 420 425 430

Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly
 435 440 445

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
 450 455 460

Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
 465 470 475 480

Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
 485 490 495

Ile Lys

<210> 185

<211> 1527

<212> DNA

<213> artificial sequence

<220>

<223> antiCD19xantiCD3 VH3VL2

<400> 185

gatatccagc tgaccagtc tccagcttct ttggctgtgt ctctagggca gagggccacc 60

atctcctgca aggccagcca aagtgttgat tatgatggtg atagttattt gaactggtac 120

caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 180
gggatccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 240
cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg 300
acgttcggtg gagggacca gctcgagatc aaaggtggtg gtggttctgg cggcggcggc 360
tccggtggtg gtggttctca ggtgcagctg cagcagtctg gggctgagct ggtgaggcct 420
gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg 480
aactgggtga agcagaggcc tggacagggt cttgagtga ttggacagat ttggcctgga 540
gatggtgata ctaactacaa tggaaagttc aagggtaaag ccactctgac tgcagacgaa 600
tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat 660
ttctgtgcaa gacgggagac tacgacggtg ggccgttatt actatgctat ggactactgg 720
ggccaaggga ccacggtcac cgtctcctcc ggaggtggtg gctccgacgt ccaactggtg 780
cagtcagggg ctgaagtga aaaacctggg gcctcagtga aggtgtcctg caaggcttct 840
ggctacaccg ctactaggta cacgatgcac tgggtaaggc aggacactgg acagggtctg 900
gaatggattg gatacattaa tcctagccgt ggttatacta attacgcaca gaagttgcag 960
ggccgcgtca caatgactac agacacttcc accagcacag cctacctgca aatgaacagc 1020
ctgaaaactg aggacactgc agtctattac tgtgcaagat attatgatga tcattactgc 1080
cttgactact ggggccaagg caccacggtc accgtctcct caggcgaagg tactagtact 1140
ggttctggtg gaagtggagg ttcaggtgga gcagacgaca ttgtactgac ccagtctcca 1200
gcaactctgt ctctgtctcc aggggagcgt gccaccctga gctgcagagc cagtcaaagt 1260
gtaagttaca tgaactggta ccagcagaag ccgggcaagg caccctaaaag atggatttat 1320
gacacatcca aagtggcttc tggagtccct gctcgcttca gtggcagtgg gtctgggacc 1380
gactactctc tcacaatcaa cagcttggag gctgaagatg ctgccactta ttactgccaa 1440
cagtggagta gtaaccgcgt cacgttcggt ggcgggacca aggtggagat caaacatcat 1500
caccatcatc attagagatc tgtcgac 1527

<210> 186

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> antiCD19xantiCD3 VH3VL2

<400> 186

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
 20 25 30
 Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
 35 40 45
 Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
 50 55 60
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65 70 75 80
 Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
 85 90 95
 Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
 100 105 110
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
 115 120 125
 Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
 130 135 140
 Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
 145 150 155 160
 Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
 165 170 175
 Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
 180 185 190
 Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
 195 200 205
 Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
 210 215 220
 Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
 225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
 245 250 255

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
 260 265 270

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ala Thr Arg Tyr Thr
 275 280 285

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
 290 295 300

Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu Gln
 305 310 315 320

Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr Leu
 325 330 335

Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 340 345 350

Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr
 355 360 365

Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly
 370 375 380

Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro
 385 390 395 400

Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
 405 410 415

Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
 420 425 430

Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly
 435 440 445

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
 450 455 460

Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln

Ile Lys

<400>	187						
gatatccagc	tgacccagtc	tccagcttct	ttggctgtgt	ctctagggca	gagggccacc		60
atctcctgca	aggccagcca	aagtgttgat	tatgatggtg	atagttattt	gaactggtac		120
caacagattc	caggacagcc	acccaaactc	ctcatctatg	atgcatccaa	tctagtttct		180
gggatcccac	ccaggtttag	tggcagtg	tctgggacag	acttcaccct	caacatccat		240
cctgtggaga	aggtggatgc	tgcaacctat	cactgtcagc	aaagtactga	ggatccgtgg		300
acgttcggtg	gagggaccaa	gctcgagatc	aaaggtggtg	gtggttctgg	cggcggcggc		360
tccggtggtg	gtggttctca	ggtgcagctg	cagcagtctg	gggctgagct	ggtgaggcct		420
gggtcctcag	tgaagatttc	ctgcaaggct	tctggctatg	cattcagtag	ctactggatg		480
aactgggtga	agcagaggcc	tggacagggt	cttgagtgga	ttggacagat	ttggcctgga		540
gatggtgata	ctaactacaa	tggaaagttc	aagggtaaag	ccactctgac	tgcagacgaa		600
tcctccagca	cagcctacat	gcaactcagc	agcctagcat	ctgaggactc	tgcggtctat		660
ttctgtgcaa	gacgggagac	tacgacggta	ggccgttatt	actatgctat	ggactactgg		720
ggccaaggga	ccacggtcac	cgtctcctcc	ggaggtggtg	gctccgacgt	ccaactggtg		780
cagtcagggg	ctgaagtga	aaaacctggg	gcctcagtga	aggtgtcctg	caaggcttct		840
ggctacaccg	ctactaggta	cacgatgcac	tgggtaaggc	aggcacctgg	acagggtctg		900
gaatggattg	gatacattaa	tcctagccgt	ggttatacta	attacgcaca	gaagttgcag		960
ggccgcgtca	caatgactac	agacacttcc	accagcacag	cctacctgca	aatgaacagc		1020
ctgaaaactg	aggacactgc	agtctattac	tgtgcaagat	attatgatga	tcattactgc		1080
cttgactact	ggggccaagg	caccacggtc	accgtctcct	caggcgaagg	tactagtact		1140
ggttctggtg	gaagtggagg	ttcaggtgga	gcagacgaca	ttgtactgac	ccagtcctcca		1200

gcaactctgt ctctgtctcc aggggagcgt gccaccctga cctgcagagc cagttcaagt 1260
 gtaagttaca tgaactggta ccagcagaag ccgggcaagg cacccaaaag atggatttat 1320
 gacacatcca aagtggcttc tggagtcctt gctcgcttca gtggcagtgg gtctgggacc 1380
 gactactctc tcacaatcaa cagcttggag gctgaagatg ctgccactta ttactgccaa 1440
 cagtggagta gtaacccgct cacgttcggt ggcgggacca aggtggagat caaacatcat 1500
 caccatcatc attagagatc tgtcgac 1527

<210> 188

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> antiCD19xantiCD3 VH3VL3

<400> 188

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
 20 25 30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
 35 40 45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
 85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
 115 120 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
 130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
 145 150 155 160
 Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
 165 170 175
 Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
 180 185 190
 Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
 195 200 205
 Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
 210 215 220
 Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
 225 230 235 240
 Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
 245 250 255
 Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
 260 265 270
 Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ala Thr Arg Tyr Thr
 275 280 285
 Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
 290 295 300
 Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Gln Lys Leu Gln
 305 310 315 320
 Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr Leu
 325 330 335
 Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 340 345 350
 Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr
 355 360 365
 Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly
 370 375 380

Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro
385 390 395 400

Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys Arg
405 410 415

Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
420 425 430

Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly
435 440 445

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
450 455 460

Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
465 470 475 480

Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
485 490 495

Ile Lys

<210> 189
<211> 1527
<212> DNA
<213> artificial sequence

<220>
<223> antiCD19xantiCD3 VH5VL1

<400> 189
gatatccagc tgaccagtc tccagcttct ttggctgtgt ctctagggca gagggccacc 60
atctcctgca aggccagcca aagtgttgat tatgatggtg atagttattt gaactggtac 120
caacagattc caggacagcc acccaaactc ctcatctatg atgcatcaa tctagtttct 180
gggatccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 240
cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg 300
acgttcggtg gagggaccaa gctcgagatc aaagtggtg gtggttctgg cggcggcggc 360
tccggtggtg gtggttctca ggtgcagctg cagcagtctg gggctgagct ggtgaggcct 420
gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg 480

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aactgggtga agcagaggcc tggacagggt cttgagtga ttggacagat ttggcctgga 540
gatgggtgata ctaactacaa tggaaagtgc aagggtaaag ccactctgac tgcagacgaa 600
tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat 660
ttctgtgcaa gacgggagac tacgacggta ggccgttatt actatgctat ggactactgg 720
ggccaaggga ccacggtcac cgtctcctcc ggaggtgggtg gctccgacgt ccaactgggtg 780
cagtcagggg ctgaagtga aaaacctggg gcctcagtga aggtgtcctg caaggcttct 840
ggctacacct ttactaggtta cacgatgcac tgggtaaggc aggcacctgg acagggctctg 900
gaatggattg gatacattaa tcctagccgt gggtatacta attacgcaga cagcgtcaag 960
ggccgcttca caatcactac agacaaatcc accagcacag cctacatgga actgagcagc 1020
ctgogttctg aggacactgc aacctattac tgtgcaagat attatgatga tcattactgc 1080
cttgactact ggggccaagg caccacgggc accgtctcct caggcgaagg tactagtact 1140
ggttctgggtg gaagtggagg ttcaggtgga gcagacgaca ttcagatgac ccagtctcca 1200
tctagcctgt ctgcatctgt cggggaccgt gtcaccatca cctgcagagc cagtcaaagt 1260
gtaagttaca tgaactggta ccagcagaag ccgggcaagg caccctaaaag atggatttat 1320
gacacatcca aagtggcttc tggagtcctt gctcgcttca gtggcagtgg gtctgggacc 1380
gactactctc tcacaatcaa cagcttgag gctgaagatg ctgccactta ttactgcca 1440
cagtgaggta gtaacccgct caggttcggt ggccgggacca aggtggagat caaacatcat 1500
caccatcatc attagagatc tgtcgac 1527

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<210> 190
<211> 498
<212> PRT
<213> artificial sequence

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<220>
<223> antiCD19xantiCD3 VH5VL1

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<400> 190

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Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1           5           10           15

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```

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20           25           30

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```

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
35           40           45

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Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
 85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
 115 120 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
 130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
 145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
 165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
 180 185 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
 195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
 210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
 225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
 245 250 255

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
 260 265 270

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr
 275 280 285

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
 290 295 300

Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys
 305 310 315 320

Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met
 325 330 335

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
 340 345 350

Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr
 355 360 365

Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly
 370 375 380

Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser Pro
 385 390 395 400

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
 405 410 415

Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
 420 425 430

Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly
 435 440 445

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
 450 455 460

Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
 465 470 475 480

Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
 485 490 495

Ile Lys

<210> 191
 <211> 1527

<212> DNA

<213> artificial sequence

<220>

<223> antiCD19xantiCD3 VH5VL2

<400> 191

gatatccagc tgacccagtc tccagcttct ttggctgtgt ctctagggca gagggccacc	60
atctcctgca aggccagcca aagtgttgat tatgatggtg atagttattt gaactggtac	120
caacagattc caggacagcc acccaaactc ctcatctatg atgcatcaa tctagtttct	180
gggatcccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat	240
cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg	300
acgttcggtg gagggaccaa gctcgagatc aaaggtggtg gtggttctgg cggcggcggc	360
tccggtggtg gtggttctca ggtgcagctg cagcagctctg gggctgagct ggtgaggcct	420
gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg	480
aactgggtga agcagaggcc tggacagggt cttgagtga ttggacagat ttggcctgga	540
gatggtgata ctaactacaa tggaaagttc aagggtaaag ccactctgac tgcagacgaa	600
tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat	660
ttctgtgcaa gacgggagac tacgacggtg ggccgttatt actatgctat ggactactgg	720
ggccaagggg ccacggtcac cgtctcctcc ggaggtggtg gctccgacgt ccaactggtg	780
cagtcagggg ctgaagtga aaaacctggg gcctcagtga aggtgtcctg caaggcttct	840
ggctacacct ttactaggtg cacgatgcac tgggtaaggc aggcacctgg acagggtctg	900
gaatggattg gatacattaa tcctagccgt ggttatacta attacgcaga cagcgtcaag	960
ggccgcttca caatcactac agacaaatcc accagcacag cctacatgga actgagcagc	1020
ctgcgttctg aggacactgc aacctattac tgtgcaagat attatgatga tcattactgc	1080
cttgactact ggggccaagg caccacggtc accgtctcct caggcgaagg tactagtact	1140
ggttctggtg gaagtggagg ttcaggtgga gcagacgaca ttgtactgac ccagtctcca	1200
gcaactctgt ctctgtctcc aggggagcgt gccaccctga gctgcagagc cagtcaaagt	1260
gtaagttaca tgaactggta ccagcagaag ccgggcaagg caccctaaag atggatttat	1320
gacacatcca aagtggcttc tggagtccct gctcgcttca gtggcagtgg gtctgggacc	1380
gactactctc tcacaatcaa cagcttgagg gctgaagatg ctgccactta ttactgccaa	1440
cagtggagta gtaacccgct cacgttcggt ggcgggacca aggtggagat caaacatcat	1500
caccatcatc attagagatc tgtcgac	1527

<210> 192
 <211> 498
 <212> PRT
 <213> artificial sequence

<220>
 <223> antiCD19xantiCD3 VH5VL2

<400> 192

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
 20 25 30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
 35 40 45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
 85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
 115 120 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
 130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
 145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
 165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
 180 185 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
 195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
 210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
 225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
 245 250 255

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
 260 265 270

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr
 275 280 285

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
 290 295 300

Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys
 305 310 315 320

Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met
 325 330 335

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
 340 345 350

Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr
 355 360 365

Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly
 370 375 380

Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro
 385 390 395 400

Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
 405 410 415

Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
 420 425 430

Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly
 435 440 445

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
 450 455 460

Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
 465 470 475 480

Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
 485 490 495

Ile Lys

<210> 193
 <211> 1527
 <212> DNA
 <213> artificial sequence

<220>
 <223> antiCD19xantiCD3 VH5VL3

<400> 193
 gatataccagc tgaccacagtc tccagcttct ttggctgtgt ctctagggca gagggccacc 60
 atctcctgca aggcagacca aagtgttgat tatgatggtg atagttattt gaactggtac 120
 caacagattc caggacagcc acccaaaactc ctcatctatg atgcatcaa tctagtttct 180
 gggatcccac ccagggttag ttggcagtggt tctgggacag acttcaccct caacatccat 240
 cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg 300
 acgttcggtg gagggaccaa gctcgagatc aaaggtggtg gtggttcttg cggcggcggc 360
 tccggtggtg gtggttctca ggtgcagctg cagcagctctg gggctgagct ggtgaggcct 420
 gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg 480
 aactgggtga agcagaggcc tggacagggt cttgagtga ttggacagat ttggcctgga 540
 gatggtgata ctaactacaa tggaaagttc aagggtaaag ccactctgac tgcagacgaa 600
 tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat 660
 ttctgtgcaa gacgggagac tacgacggta ggccgttatt actatgctat ggactactgg 720
 ggccaaggga ccacgggtcac cgtctcctcc ggaggtggtg gctccgacgt ccaactggtg 780
 cagtcagggg ctgaagtga aaaacctggg gcctcagtga aggtgtcctg caaggcttct 840
 ggctacacct ttactaggta cacgatgcac tgggtaaggc aggcacctgg acagggtctg 900

gaatggattg gatacattaa tcctagccgt gggtatacta attacgcaga cagcgtcaag 960
 ggccgcttca caatcactac agacaaatcc accagcacag cctacatgga actgagcagc 1020
 ctgcgttctg aggacactgc aacctattac tgtgcaagat attatgatga tcattactgc 1080
 cttgactact ggggccaaagg caccacggtc accgtctcct caggcgaagg tactagtact 1140
 gggttctggtg gaagtggagg ttcagggtga gcagacgaca ttgtactgac ccagtctcca 1200
 gcaactctgt ctctgtctcc aggggagcgt gccaccctga cctgcagagc cagttcaagt 1260
 gtaagttaca tgaactggta ccagcagaag ccgggcaagg caccctaaaag atggatttat 1320
 gacacatcca aagtggcttc tggagtcctt gctcgcttca gtggcagtgg gtctgggacc 1380
 gactactctc tcacaatcaa cagcttggag gctgaagatg ctgccactta ttactgccaa 1440
 cagtggagta gtaaccgct cacgttcggt ggccgggacca aggtggagat caaacatcat 1500
 caccatcatc attagagatc tgtcgac 1527

<210> 194
 <211> 498
 <212> PRT
 <213> artificial sequence

<220>
 <223> antiCD19xantiCD3 VH5VL3

<400> 194.

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
 20 25 30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
 35 40 45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
 85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly

100	105	110
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val 115 120 125		
Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val 130 135 140		
Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met 145 150 155 160		
Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln 165 170 175		
Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly 180 185 190		
Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln 195 200 205		
Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg 210 215 220		
Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp 225 230 235 240		
Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp 245 250 255		
Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser 260 265 270		
Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr 275 280 285		
Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly 290 295 300		
Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys 305 310 315 320		
Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met 325 330 335		

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
 340 345 350

Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr
 355 360 365

Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly
 370 375 380

Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro
 385 390 395 400

Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys Arg
 405 410 415

Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
 420 425 430

Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly
 435 440 445

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
 450 455 460

Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
 465 470 475 480

Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
 485 490 495

Ile Lys

<210> 195

<211> 1527

<212> DNA

<213> artificial sequence

<220>

<223> antiCD19xantiCD3 VH7VL1

<400> 195

gatatccagc tgaccagtc tccagcttct ttggctgtgt ctctagggca gagggccacc 60

atctcctgca aggccagcca aagtgttgat tatgatggtg atagttattt gaactggtac 120

caacagattc caggacagcc acccaaaactc ctcatttatg atgcatccaa tctagtttct 180

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gggatccac ccaggttttag tggcagtggg tctgggacag acttcaccct caacatccat 240
cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg 300
acgttcggtg gagggaccaa gctcgagatc aaaggtggtg gtggttctgg cggcggcggc 360
tccggtggtg gtggttctca ggtgcagctg cagcagtctg gggctgagct ggtgaggcct 420
gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg 480
aactgggtga agcagaggcc tggacagggt cttgagtgga ttggacagat ttggcctgga 540
gatggtgata ctaactacaa tggaaagttc aagggtaaag ccactctgac tgcagacgaa 600
tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat 660
ttctgtgcaa gacgggagac tacgacggta ggccgttatt actatgctat ggactactgg 720
ggccaaggga ccacggtcac cgtctcctcc ggaggtggtg gctccgacgt ccaactggtg 780
cagtcagggg ctgaagtga aaaacctggg gcctcagtga aggtgtcctg caaggcttct 840
ggctacacct ttactaggta cacgatgcac tgggtaaggc aggcacctgg acagggtctg 900
gaatggattg gatacattaa tcctagccgt gggtatacta attacaatca gaagttcaag 960
gaccggtca caatcactac agacaaatcc accagcacag cctacatgga actgagcagc 1020
ctgcgttctg aggacactgc agtctattac tgtgcaagat attatgatga tcattactgc 1080
cttgactact gggggccaagg caccacggtc accgtctcct caggcgaagg tactagtact 1140
ggttctggtg gaagtggagg ttcagggtga gcagacgaca ttcagatgac ccagtctcca 1200
tctagcctgt ctgcatctgt cggggaccgt gtcaccatca cctgcagagc cagtcaaagt 1260
gtaagttaca tgaactggta ccagcagaag ccgggcaagg cacccaaaag atggatttat 1320
gacacatcca aagtggcttc tggagtccct gctcgcttca gtggcagtgg gtctgggacc 1380
gactactctc tcacaatcaa cagcttggag gctgaagatg ctgccactta ttactgccaa 1440
cagtgagta gtaaccgct cacgttcggt ggcgggacca aggtggagat caaacatcat 1500
caccatcatc attagagatc tgtcgac 1527

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<210> 196

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> antiCD19xantiCD3 VH7VL1

<400> 196

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
115 120 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
180 185 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp

245	250	255
Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser		
260	265	270
Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr		
275	280	285
Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly		
290	295	300
Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys		
305	310	315
Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met		
325	330	335
Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala		
340	345	350
Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr		
355	360	365
Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly		
370	375	380
Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser Pro		
385	390	395
Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg		
405	410	415
Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly		
420	425	430
Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly		
435	440	445
Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu		
450	455	460
Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln		
465	470	475
		480

Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
 485 490 495

Ile Lys

<210> 197
 <211> 1527
 <212> DNA
 <213> artificial sequence

<220>
 <223> antiCD19xantiCD3 VH7VL2

<400> 197
 gatatccagc tgaccagtc tccagcttct ttggctgtgt ctctagggca gagggccacc 60
 atctcctgca aggccagcca aagtgttgat tatgatgggtg atagttattt gaactggtac 120
 caacagattc caggacagcc acccaaactc ctcatctatg atgcatcaa tctagtttct 180
 gggatcccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 240
 cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg 300
 acgttcggtg gagggaccaa gctcgagatc aaaggtggtg gtggttcttg cggcggcggc 360
 tccggtggtg gtggttctca ggtgcagctg cagcagctctg gggctgagct ggtgaggcct 420
 gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg 480
 aactgggtga agcagaggcc tggacagggt cttgagtga ttggacagat ttggcctgga 540
 gatggtgata ctaactacaa tggaaagttc aagggtaaag ccactctgac tgcagacgaa 600
 tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat 660
 ttctgtgcaa gacgggagac tacgacggtg ggccgttatt actatgctat ggactactgg 720
 ggccaaggga ccacggtcac cgtctcctcc ggaggtggtg gctccgacgt ccaactggtg 780
 cagtcagggg ctgaagtga aaaacctggg gcctcagtga aggtgtcctg caaggcttct 840
 ggctacacct ttactaggtg cacgatgcac tgggtaaggc aggcacctgg acagggtctg 900
 gaatggattg gatacattaa tcctagccgt gggtatacta attacaatca gaagttcaag 960
 gaccgcgtca caatcactac agacaaatcc accagcacag cctacatgga actgagcagc 1020
 ctgcgttctg aggacactgc agtctattac tgtgcaagat attatgatga tcattactgc 1080
 cttgactact ggggccaaagg caccacggtc accgtctcct caggcgaagg tactagtact 1140
 ggttctggtg gaagtggagg ttcaggtgga gcagacgaca ttgtactgac ccagtctcca 1200
 gcaactctgt ctctgtctcc aggggagcgt gccaccctga gctgcagagc cagtcaaagt 1260

gtaagttaca tgaactggta ccagcagaag ccgggcaagg cacccaaaag atggatttat 1320
gacacatcca aagtggcttc tggagtcctt gctcgcttca gtggcagtgg gtctgggacc 1380
gactactctc tcacaatcaa cagcttggag gctgaagatg ctgccactta ttactgccaa 1440
cagtggagta gtaacccgct cacgttcggt ggcgggacca aggtggagat caaacatcat 1500
caccatcatc attagagatc tgtcgac 1527

<210> 198
<211> 498
<212> PRT
<213> artificial sequence

<220>
<223> antiCD19xantiCD3 VH7VL2

<400> 198

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
115 120 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
 165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
 180 185 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
 195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
 210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
 225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
 245 250 255

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
 260 265 270

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr
 275 280 285

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
 290 295 300

Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys
 305 310 315 320

Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met
 325 330 335

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 340 345 350

Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr
 355 360 365

Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly
 370 375 380

Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro

Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
485 490 495

Ile Lys

```
<210> 199
<211> 1527
<212> DNA
<213> artificial sequence
```

```
<220>
<223> antiCD19xantiCD3 VH7VL3
```

<400> 199						
gatatccagc	tgacccagtc	tccagcttct	ttggctgtgt	ctctagggca	gagggccacc	60
atctcctgca	aggccagcca	aagtgttgat	tatgatggtg	atagttattt	gaactggtac	120
caacagattc	caggacagcc	acccaaactc	ctcatctatg	atgcatccaa	tctagtttct	180
gggatcccac	ccaggtttag	tggcagtggg	tctgggacag	acttcaccct	caacatccat	240
cctgtggaga	aggtggatgc	tgcaacctat	cactgtcagc	aaagtactga	ggatccgtgg	300
acgttcgggtg	gagggaccaa	gctcgagatc	aaaggtggtg	gtggttctgg	cggcggcggc	360
tccggtggtg	gtggttctca	ggtgcagctg	cagcagtctg	gggctgagct	ggtgaggcct	420
gggtcctcag	tgaagatttc	ctgcaaggct	tctggctatg	cattcagtag	ctactggatg	480
aactgggtga	agcagaggcc	tggacagggc	cttgagtgga	ttggacagat	ttggcctgga	540
gatggtgata	ctaactacaa	tggaaagttc	aagggtaaag	ccactctgac	tgcagacqaa	600


```

tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat   660
ttctgtgcaa gacgggagac tacgacggta ggccgttatt actatgctat ggactactgg   720
ggccaagggg ccacggtcac cgtctcctcc ggagggtggtg gctccgacgt ccaactggtg   780
cagtcagggg ctgaagtga aaaaacctggg gcctcagtga aggtgtcctg caaggcttct   840
ggctacacct ttactaggtta cacgatgcac tgggtaaggc aggcaçctgg acagggtctg   900
gaatggattg gatacattaa tcctagccgt ggttatacta attacaatca gaagttcaag   960
gaccgcgtca caatcactac agacaaatcc accagcacag cctacatgga actgagcagc  1020
ctgcgttctg aggacactgc agtctattac tgtgcaagat attatgatga tcattactgc  1080
cttgactact ggggccaaagg caccacggtc accgtctcct caggcgaagg tactagtact  1140
ggttctggtg gaagtggagg ttcagggtga gcagacgaca ttgtactgac ccagtctcca  1200
gcaactctgt ctctgtctcc aggggagcgt gccaccctga cctgcagagc cagttcaagt  1260
gtaagttaca tgaactggta ccagcagaag ccgggcaagg caccctaaaag atggatttat  1320
gacacatcca aagtggcttc tggagtcctt gctcgcttca gtggcagtgg gtctgggacc  1380
gactactctc tcacaatcaa cagcttggag gctgaagatg ctgccactta ttactgcca  1440
cagtgaggta gtaaccgct caggttcggt ggcgggacca aggtggagat caaacatcat  1500
caccatcatc attagagatc tgtcgac                                     1527

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<210> 200

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> antiCD19xantiCD3 VH7VL3

<400> 200

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Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1           5           10           15

```

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Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
          20           25           30

```

```

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
          35           40           45

```

```

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
          50           55           60

```

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
115 120 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
180 185 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
245 250 255

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
260 265 270

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr
275 280 285

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
290 295 300

Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys
 305 310 315 320

Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met
 325 330 335

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 340 345 350

Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr
 355 360 365

Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly
 370 375 380

Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro
 385 390 395 400

Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys Arg
 405 410 415

Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
 420 425 430

Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly
 435 440 445

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
 450 455 460

Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
 465 470 475 480

Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
 485 490 495

Ile Lys

<210> 201

<211> 45

<212> DNA

<213> artificial sequence

<220>

<223> standard linker

<400> 201

ggtaggtggtg gttctggcgg cggcggctcc ggtggtggtg gttct

45

<210> 202

<211> 54

<212> DNA

<213> artificial sequence

<220>

<223> deimmunized linker

<400> 202

ggcgaaggta ctagtactgg ttctggtgga agtggaggtt caggtggagc agac

54

<210> 203

<211> 1494

<212> DNA

<213> artificial sequence

<220>

<223> antiCD19xantiCD3

<400> 203

gatatccagc tgaccagtc tccagcttct ttggctgtgt ctctagggca gagggccacc 60

atctcctgca aggccagcca aagtgttgat tatgatggtg atagtatttt gaactgggtac 120

caacagattc caggacagcc acccaaactc ctcatctatg atgcatcaa tctagtttct 180

gggatccac ccaggttttag tggcagtggtg tctgggacag acttcaccct caacatccat 240

cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg 300

acgttcggtg gagggaccaa gctcgagatc aaaggtggtg gtggttctgg cggcggcggc 360

tccggtggtg gtggttctca ggtgcagctg cagcagtctg gggctgagct ggtgaggcct 420

gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg 480

aactgggtga agcagaggcc tggacagggt cttgagtgga ttggacagat ttggcctgga 540

gatggtgata ctaactacaa tggaaagttc aagggtaaag ccactctgac tgcagacgaa 600

tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat 660

ttctgtgcaa gacgggagac tacgacggta ggccgttatt actatgctat ggactactgg 720

ggccaaggga ccacggtcac cgtctcctcc ggaggtggtg gatccgatat caaactgcag 780

cagtcagggg ctgaactggc aagacctggg gcctcagtga agatgtcctg caagacttct 840

ggctacacct ttactaggtg cacgatgcac tgggtaaaac agaggcctgg acagggctctg 900

gaatggattg gatacattaa tcctagccgt gggtatacta attacaatca gaagttcaag 960

gacaaggcca cattgactac agacaaatcc tccagcacag cctacatgca actgagcagc 1020
 ctgacatctg aggactctgc agtctattac tgtgcaagat attatgatga tcattactgc 1080
 cttgactact ggggccaagg caccactctc acagtctcct cagtcgaagg tggaagtgga 1140
 ggttctgggtg gaagtggagg ttcaggtgga gtcgacgaca ttcagctgac ccagtctcca 1200
 gcaatcatgt ctgcatctcc aggggagaag gtcacatga cctgcagagc cagttcaagt 1260
 gtaagttaca tgaactggta ccagcagaag tcaggcacct cccccaaaag atggatttat 1320
 gacacatcca aagtggcttc tggagtcctt tatcgcttca gtggcagtggt gtctgggacc 1380
 tcatactctc tcacaatcag cagcatggag gctgaagatg ctgccactta ttactgcca 1440
 cagtgaggta gtaaccgct cacgttcggt gctgggacca agctggagct gaaa 1494

<210> 204
 <211> 498
 <212> PRT
 <213> artificial sequence

<220>
 <223> antiCD19xantiCD3

<400> 204

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
 20 25 30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
 35 40 45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
 85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val

115		120		125	
Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val					
130		135		140	
Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met					
145		150		155	160
Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln					
	165		170		175
Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly					
	180		185		190
Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln					
	195		200		205
Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg					
	210		215		220
Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp					
225		230		235	240
Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp					
	245		250		255
Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser					
	260		265		270
Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr Thr					
	275		280		285
Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly					
	290		295		300
Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys					
305		310		315	320
Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met					
	325		330		335
Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala					
	340		345		350

Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr
 355 360 365

Thr Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly Gly Ser Gly Gly
 370 375 380

Ser Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu Thr Gln Ser Pro
 385 390 395 400

Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg
 405 410 415

Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly
 420 425 430

Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly
 435 440 445

Val Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
 450 455 460

Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
 465 470 475 480

Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu
 485 490 495

Leu Lys

<210> 205

<211> 1476

<212> DNA

<213> artificial sequence

<220>

<223> CCR5xanti-CD3 VH5VL1

<400> 205

gacattatcc tgatccaatc tccaccttct ttggctgtgt ctctagggca gagggccacc 60

atctcctgca gaaccagcga aaatgttgac ggatacggca ttagttttat aaactggtac 120

caacagaagc caggacagcc acccaaaactc ctcatttatg ctgcatccca ccaaggatcc 180

ggggtccttg ccagatttag tggcagtggg tctgggacag acttcagcct caacatccat 240

cctttggagg aggatgatac tgcaatgtat ttctgtcacc aaagtaagaa gggtccgtgg 300

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acgttcggtg gaggcaccaa gctggaaatc aaaggtggtg gtggttcttg cggcggcggc 360
tccggtggtg gtggttctca gctggagcag tctggacctg aactgaagaa gcctggagag 420
acagtcacga tctcctgcaa ggcttctggg tataccttca cgaagttcgg aatgaactgg 480
gtgaagcagg ctccaggaaa gggtttaaag tggatgggct ggatacacac ctccactgga 540
gagccaacat attctgatga cttcaaggga cggtttgctt tctctttgga aacgtctgcc 600
agcactgcct atttgcggtat caacaacctc aaaaatgagg acatggctaa atacttctgt 660
gccagaggtg gtccttacgt aaggggtgct ttggactact ggggtcaagg aacctcagtc 720
accgtctcct ccggaggtgg tggatccgac gtccaactgg tgcagtcagg ggctgaagtg 780
aaaaaacctg gggcctcagt gaaggtgtcc tgcaaggctt ctggctacac ctttactagg 840
tacacgatgc actgggtaag gcaggcacct ggacagggtc tggaatggat tggatacatt 900
aatcctagcc gtggttatac taattacgca gacagcgtca agggccgctt cacaatcact 960
acagacaaat ccaccagcac agcctacatg gaactgagca gcctgcgttc tgaggacact 1020
gcaacctatt actgtgcaag atattatgat gatcattact gccttgacta ctggggccaa 1080
ggcaccacgg tcaccgtctc ctcaggcgaa ggtactagta ctggttcttg tggaagtgga 1140
ggttcaggtg gagcagacga cattcagatg acccagtctc catctagcct gtctgcatct 1200
gtcggggacc gtgtcaccat cacctgcaga gccagtcaaa gtgtaagtta catgaactgg 1260
taccagcaga agccgggcaa ggcacccaaa agatggattt atgacacatc caaagtggct 1320
tctggagtcc ctgctcgctt cagtggcagt gggctctggga ccgactactc tctcacaatc 1380
aacagcttgg aggctgaaga tgctgccact tattactgcc aacagtggag tagtaaccgc 1440
ctcacgttcg gtggcgggac caaggtggag atcaaaa 1476

```

<210> 206

<211> 492

<212> PRT

<213> artificial sequence

<220>

<223> CCR5xanti-CD3 VH5VL1

<400> 206

```

Asp Ile Ile Leu Ile Gln Ser Pro Pro Ser Leu Ala Val Ser Leu Gly
1           5           10           15

```

```

Gln Arg Ala Thr Ile Ser Cys Arg Thr Ser Glu Asn Val Asp Gly Tyr
          20           25           30

```


Gly Ile Ser Phe Ile Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser His Gln Gly Ser Gly Val Pro Ala
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His
 65 70 75 80

Pro Leu Glu Glu Asp Asp Thr Ala Met Tyr Phe Cys His Gln Ser Lys
 85 90 95

Lys Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Leu
 115 120 125

Glu Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr Val Thr Ile
 130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Lys Phe Gly Met Asn Trp
 145 150 155 160

Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met Gly Trp Ile His
 165 170 175

Thr Ser Thr Gly Glu Pro Thr Tyr Ser Asp Asp Phe Lys Gly Arg Phe
 180 185 190

Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr Leu Arg Ile Asn
 195 200 205

Asn Leu Lys Asn Glu Asp Met Ala Lys Tyr Phe Cys Ala Arg Gly Gly
 210 215 220

Pro Tyr Val Arg Gly Ala Leu Asp Tyr Trp Gly Gln Gly Thr Ser Val
 225 230 235 240

Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val Gln Ser
 245 250 255

Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
 260 265 270

Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln
 275 280 285

Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg
 290 295 300

Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Thr
 305 310 315 320

Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg
 325 330 335

Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His
 340 345 350

Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 355 360 365

Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
 370 375 380

Ala Asp Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
 385 390 395 400

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser
 405 410 415

Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp
 420 425 430

Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser
 435 440 445

Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu
 450 455 460

Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro
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Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 485 490

<210> 207
 <211> 1476

<212> DNA

<213> artificial sequence

<220>

<223> CCR5xanti-CD3 VH5VL2

<400> 207

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caacagaagc caggacagcc acccaaactc ctcatctatg ctgcatccca ccaaggatcc      180
ggggtccctg ccagatttag tggcagtggg tctgggacag acttcagcct caacatccat      240
cctttggagg aggatgatac tgcaatgtat ttctgtcacc aaagtaagaa ggttccgtgg      300
acgttcggtg gaggcaccaa gctggaaatc aaaggtggtg gtggttctgg cggcggcggc      360
tccggtggtg gtggttctca gctggagcag tctggacctg aactgaagaa gcctggagag      420
acagtcacga tctcctgcaa ggcttctggg tataccttca cgaagtccgg aatgaactgg      480
gtgaagcagg ctccaggaaa gggtttaaag tggatgggct ggatacacac ctccactgga      540
gagccaacat attctgatga cttcaaggga cggtttgcct tctctttgga aacgtctgcc      600
agcactgcct atttgcggat caacaacctc aaaaatgagg acatggctaa atacttctgt      660
gccagagggtg gtccttacgt aaggggtgct ttggactact ggggtcaagg aacctcagtc      720
accgtctcct ccggagggtg tggatccgac gtccaactgg tgcagtcagg ggctgaagtg      780
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acagacaaat ccaccagcac agcctacatg gaactgagca gcctgcgttc tgaggacact     1020
gcaacctatt actgtgcaag atattatgat gatcattact gccttgacta ctggggccaa     1080
ggcaccacgg tcaccgtctc ctcaggcgaa ggtactagta ctggttctgg tggaagtgga     1140
ggttcagggtg gagcagacga cattgtactg acccagtctc cagcaactct gtctctgtct     1200
ccaggggagc gtgccaccct gagctgcaga gccagtcaaa gtgtaagtta catgaactgg     1260
taccagcaga agccgggcaa ggcacccaaa agatggattt atgacacatc caaagtggct     1320
tctggagtcc ctgctcgctt cagtggcagt gggctctggga ccgactactc tctcacaatc     1380
aacagcttgg aggctgaaga tgctgccact tattactgcc aacagtggag tagtaaccog     1440
ctcacgttcg gtggcgggac caaggtggag atcaaaa                                1476
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<210> 208

<211> 492

<212> PRT

<213> artificial sequence

<220>

<223> CCR5xanti-CD3 VH5VL2

<400> 208

Asp Ile Ile Leu Ile Gln Ser Pro Pro Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Arg Thr Ser Glu Asn Val Asp Gly Tyr
 20 25 30

Gly Ile Ser Phe Ile Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser His Gln Gly Ser Gly Val Pro Ala
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His
 65 70 75 80

Pro Leu Glu Glu Asp Asp Thr Ala Met Tyr Phe Cys His Gln Ser Lys
 85 90 95

Lys Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Leu
 115 120 125

Glu Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr Val Thr Ile
 130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Lys Phe Gly Met Asn Trp
 145 150 155 160

Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met Gly Trp Ile His
 165 170 175

Thr Ser Thr Gly Glu Pro Thr Tyr Ser Asp Asp Phe Lys Gly Arg Phe
 180 185 190

Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr Leu Arg Ile Asn
 195 200 205

Asn Leu Lys Asn Glu Asp Met Ala Lys Tyr Phe Cys Ala Arg Gly Gly
 210 215 220

Pro Tyr Val Arg Gly Ala Leu Asp Tyr Trp Gly Gln Gly Thr Ser Val
 225 230 235 240

Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val Gln Ser
 245 250 255

Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
 260 265 270

Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln
 275 280 285

Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg
 290 295 300

Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Thr
 305 310 315 320

Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg
 325 330 335

Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His
 340 345 350

Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 355 360 365

Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
 370 375 380

Ala Asp Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser
 385 390 395 400

Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser
 405 410 415

Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp
 420 425 430

Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser

435

440

445

Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu
 450 455 460

Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro
 465 470 475 480

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 485 490

<210> 209

<211> 1476

<212> DNA

<213> artificial sequence

<220>

<223> CCR5xanti-CD3 VH5VL3

<400> 209

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 caacagaagc caggacagcc acccaaactc ctcatctatg ctgcatccca ccaaggatcc 180
 ggggtccctg ccagatttag tggcagtggg tctgggacag acttcagcct caacatccat 240
 cctttggagg aggatgatac tgcaatgtat ttctgtcacc aaagtaagaa ggttccgtgg 300
 acgttcggtg gaggcaccaa gctggaaatc aaagggtggtg gtggttctgg cggcggcggc 360
 tccggtggtg gtggttctca gctggagcag tctggacctg aactgaagaa gcctggagag 420
 acagtcacga tctcctgcaa ggcttctggg tataccttca cgaagtctcg aatgaactgg 480
 gtgaagcagg ctccaggaaa gggtttaaaag tggatgggct ggatacacac ctccactgga 540
 gagccaacat attctgatga cttcaaggga cggtttgcct tctctttgga aacgtctgcc 600
 agcactgcct atttgcgat caacaacctc aaaaatgagg acatggctaa atacttctgt 660
 gccagaggtg gtccttacgt aaggggtgct ttggactact ggggtcaagg aacctcagtc 720
 accgtctcct ccggaggtgg tggatccgac gtccaactgg tgcagtcagg ggctgaagtg 780
 aaaaaacctg gggcctcagt gaagggtgtc tgcaaggctt ctggctacac ctttactagg 840
 tacacgatgc actgggtaag gcaggcacct ggacagggtc tggaatggat tggatacatt 900
 aatcctagcc gtggttatac taattacgca gacagcgtca agggccgctt cacaatcact 960
 acagacaaat ccaccagcac agcctacatg gaactgagca gcctgcgttc tgaggacact 1020
 gcaacctatt actgtgcaag atattatgat gatcattact gccttgacta ctggggccaa 1080

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ggcaccacgg tcaccgtctc ctcaggcgaa ggtactagta ctggttctgg tggaagtgga 1140
ggttcaggtg gagcagacga cattgtactg acccagtctc cagcaactct gtctctgtct 1200
ccaggggagc gtgccaccct gacctgcaga gccagttcaa gtgtaagtta catgaactgg 1260
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tctggagtcc ctgctcgctt cagtggcagt gggctctggga ccgactactc tctcacaatc 1380
aacagcttgg aggctgaaga tgctgccact tattactgcc aacagtggag tagtaaccog 1440
ctcacgttcg gtggcgggac caaggtggag atcaaa 1476

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<210> 210

<211> 492

<212> PRT

<213> artificial sequence

<220>

<223> CCR5xanti-CD3 VH5VL3

<400> 210

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Asp Ile Ile Leu Ile Gln Ser Pro Pro Ser Leu Ala Val Ser Leu Gly
1.          5          10          15

```

```

Gln Arg Ala Thr Ile Ser Cys Arg Thr Ser Glu Asn Val Asp Gly Tyr
          20          25          30

```

```

Gly Ile Ser Phe Ile Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
          35          40          45

```

```

Lys Leu Leu Ile Tyr Ala Ala Ser His Gln Gly Ser Gly Val Pro Ala
          50          55          60

```

```

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His
65          70          75          80

```

```

Pro Leu Glu Glu Asp Asp Thr Ala Met Tyr Phe Cys His Gln Ser Lys
          85          90          95

```

```

Lys Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
          100          105          110

```

```

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Leu
          115          120          125

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Glu Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr Val Thr Ile

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130		135		140
Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Lys Phe Gly Met Asn Trp				
145		150		155 160
Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met Gly Trp Ile His				
		165		170 175
Thr Ser Thr Gly Glu Pro Thr Tyr Ser Asp Asp Phe Lys Gly Arg Phe				
		180		185 190
Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr Leu Arg Ile Asn				
		195		200 205
Asn Leu Lys Asn Glu Asp Met Ala Lys Tyr Phe Cys Ala Arg Gly Gly				
		210		215 220
Pro Tyr Val Arg Gly Ala Leu Asp Tyr Trp Gly Gln Gly Thr Ser Val				
		225		230 235 240
Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val Gln Ser				
		245		250 255
Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys				
		260		265 270
Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln				
		275		280 285
Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg				
		290		295 300
Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Thr				
		305		310 315 320
Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg				
		325		330 335
Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His				
		340		345 350
Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser				
		355		360 365

Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
370 375 380

Ala Asp Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser
385 390 395 400

Pro Gly Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser
405 410 415

Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp
420 425 430

Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser
435 440 445

Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu
450 455 460

Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro
465 470 475 480

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
485 490

<210> 211

<211> 1476

<212> DNA

<213> artificial sequence

<220>

<223> CCR5xanti-CD3 VH7VL1

<400> 211

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caacagaagc caggacagcc acccaaaactc ctcattctatg ctgcatccca ccaaggatcc	180
gggggtccctg ccagatttag tggcagtggg tctgggacag acttcagcct caacatccat	240
cctttggagg aggatgatac tgcaatgtat ttctgtcacc aaagtaagaa ggttccgtgg	300
acgttcggtg gaggcaccaa gctggaaatc aaaggtggtg gtggttctgg cggcggcggc	360
tccggtggtg gtggttctca gctggagcag tctggacctg aactgaagaa gcctggagag	420
acagtcacga tctcctgcaa ggcttctggg tataccttca cgaagtccgg aatgaactgg	480
gtgaagcagg ctccaggaaa gggtttaaag tggatgggct ggatacacac ctccactgga	540

gagccaacat attctgatga cttcaaggga cggtttgct tctctttgga aacgtctgcc 600
 agcactgcct atttgcgat caacaacctc aaaaatgagg acatggctaa atacttctgt 660
 gccagaggtg gtccttacgt aaggggtgct ttggactact ggggtcaagg aacctcagtc 720
 accgtctcct ccggaggtgg tggatccgac gtccaactgg tgcagtcagg ggctgaagtg 780
 aaaaaacctg gggcctcagt gaaggtgtcc tgcaaggctt ctggctacac ctttactagg 840
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 aatcctagcc gtggttatac taattacaat cagaagttca aggaccgcgt cacaatcact 960
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 gtcggggacc gtgtcaccat cacctgcaga gccagtcaaa gtgtaagtta catgaactgg 1260
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 tctggagtcc ctgctcgctt cagtggcagt gggctctggga ccgactactc tctcacaatc 1380
 aacagcttgg aggctgaaga tgctgccact tattactgcc aacagtggag tagtaaccgcg 1440
 ctcacgttcg gtggcgggac caaggtggag atcaaa 1476

<210> 212

<211> 492

<212> PRT

<213> artificial sequence

<220>

<223> CCR5xanti-CD3 VH7VL1

<400> 212

Asp Ile Ile Leu Ile Gln Ser Pro Pro Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Arg Thr Ser Glu Asn Val Asp Gly Tyr
 20 25 30

Gly Ile Ser Phe Ile Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser His Gln Gly Ser Gly Val Pro Ala
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His
65 70 75 80

Pro Leu Glu Glu Asp Asp Thr Ala Met Tyr Phe Cys His Gln Ser Lys
85 90 95

Lys Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Leu
115 120 125

Glu Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr Val Thr Ile
130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Lys Phe Gly Met Asn Trp
145 150 155 160

Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met Gly Trp Ile His
165 170 175

Thr Ser Thr Gly Glu Pro Thr Tyr Ser Asp Asp Phe Lys Gly Arg Phe
180 185 190

Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr Leu Arg Ile Asn
195 200 205

Asn Leu Lys Asn Glu Asp Met Ala Lys Tyr Phe Cys Ala Arg Gly Gly
210 215 220

Pro Tyr Val Arg Gly Ala Leu Asp Tyr Trp Gly Gln Gly Thr Ser Val
225 230 235 240

Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val Gln Ser
245 250 255

Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
260 265 270

Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln
275 280 285

Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg
290 295 300

Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr
305 310 315 320

Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg
325 330 335

Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His
340 345 350

Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
355 360 365

Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
370 375 380

Ala Asp Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
385 390 395 400

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser
405 410 415

Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp
420 425 430

Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser
435 440 445

Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu
450 455 460

Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro
465 470 475 480

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
485 490

<210> 213

<211> 1476

<212> DNA

<213> artificial sequence

<220>

<223> CCR5xanti-CD3 VH7VL2

<400> 213

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caacagaagc caggacagcc acccaaaactc ctcatctatg ctgcatccca ccaaggatcc 180
ggggtccctg ccagatttag tggcagtggg tctgggacag acttcagcct caacatccat 240
cctttggagg aggatgatac tgcaatgtat ttctgtcacc aaagtaagaa ggttccgtgg 300
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tccggtggtg gtggttctca gctggagcag tctggacctg aactgaagaa gcctggagag 420
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gtgaagcagg ctccaggaaa gggtttaaag tggatgggct ggatacacac ctccactgga 540
gagccaacat attctgatga cttcaaggga cggtttgcct tctctttgga aacgtctgcc 600
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gccagaggtg gtccttacgt aaggggtgct ttggactact ggggtcaagg aacctcagtc 720
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aacagcttgg aggctgaaga tgctgccact tattactgcc aacagtggag tagtaaccg 1440
ctcacgttcg gtggcgggac caaggtggag atcaaa 1476

<210> 214

<211> 492

<212> PRT

<213> artificial sequence

<220>

<223> CCR5xanti-CD3 VH7VL2

<400> 214

Asp Ile Ile Leu Ile Gln Ser Pro Pro Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Arg Thr Ser Glu Asn Val Asp Gly Tyr
20 25 30

Gly Ile Ser Phe Ile Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser His Gln Gly Ser Gly Val Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His
65 70 75 80

Pro Leu Glu Glu Asp Asp Thr Ala Met Tyr Phe Cys His Gln Ser Lys
85 90 95

Lys Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Leu
115 120 125

Glu Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr Val Thr Ile
130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Lys Phe Gly Met Asn Trp
145 150 155 160

Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met Gly Trp Ile His
165 170 175

Thr Ser Thr Gly Glu Pro Thr Tyr Ser Asp Asp Phe Lys Gly Arg Phe
180 185 190

Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr Leu Arg Ile Asn
195 200 205

Asn Leu Lys Asn Glu Asp Met Ala Lys Tyr Phe Cys Ala Arg Gly Gly
210 215 220

Pro Tyr Val Arg Gly Ala Leu Asp Tyr Trp Gly Gln Gly Thr Ser Val
225 230 235 240

Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val Gln Ser
 245 250 255

Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
 260 265 270

Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln
 275 280 285

Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg
 290 295 300

Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr
 305 310 315 320

Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg
 325 330 335

Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His
 340 345 350

Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 355 360 365

Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
 370 375 380

Ala Asp Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser
 385 390 395 400

Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser
 405 410 415

Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp
 420 425 430

Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser
 435 440 445

Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu
 450 455 460

Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro

465

470

475

480

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 485 490

<210> 215

<211> 1476

<212> DNA

<213> artificial sequence

<220>

<223> CCR5xanti-CD3 VH7VL3

<400> 215

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caacagaagc caggacagcc acccaaactc ctcatctatg ctgcatccca ccaaggatcc      180
ggggtccctg ccagatttag tggcagtggg tctgggacag acttcagcct caacatccat      240
cctttggagg aggatgatac tgcaatgtat ttctgtcacc aaagtaagaa ggttccgtgg      300
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tccggtggtg gtggttctca gctggagcag tctggacctg aactgaagaa gcctggagag      420
acagtcacga tctcctgcaa ggcttctggg tataccttca cgaagttcgg aatgaactgg      480
gtgaagcagg ctccaggaaa gggtttaaag tggatgggct ggatacacac ctccactgga      540
gagccaacat attctgatga cttcaaggga cggtttgcct tctctttgga aacgtctgcc      600
agcactgcct atttgcgat caacaacctc aaaaatgagg acatggctaa atacttctgt      660
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tacacgatgc actgggtaag gcaggcacct ggacagggtc tggaatggat tggatacatt      900
aatcctagcc gtggttatac taattacaat cagaagttca aggaccgcgt cacaatcact      960
acagacaaat ccaccagcac agcctacatg gaactgagca gcctgcgttc tgaggacact     1020
gcagtctatt actgtgcaag atattatgat gatcattact gccttgacta ctggggccaa     1080
ggcaccacgg tcaccgtctc ctgaggcgaa ggtactagta ctggttctgg tggaagtgga     1140
ggttcaggtg gagcagacga cattgtactg acccagtctc cagcaactct gtctctgtct     1200
ccagggggagc gtgccaccct gacctgcaga gccagttcaa gtgtaagtta catgaactgg     1260
taccagcaga agccggggcaa ggcacccaaa agatggattt atgacacatc caaagtggct     1320

```


tctggagtcc ctgctcgctt cagtggcagt gggctctggga ccgactactc tctcacaatc 1380
 aacagcttgg aggctgaaga tgctgccact tattactgcc aacagtggag tagtaacccg 1440
 ctcacgttcg gtggcgggac caaggtggag atcaaa 1476

<210> 216
 <211> 492
 <212> PRT
 <213> artificial sequence

<220>
 <223> CCR5xanti-CD3 VH7VL3

<400> 216

Asp Ile Ile Leu Ile Gln Ser Pro Pro Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Arg Thr Ser Glu Asn Val Asp Gly Tyr
 20 25 30

Gly Ile Ser Phe Ile Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser His Gln Gly Ser Gly Val Pro Ala
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His
 65 70 75 80

Pro Leu Glu Glu Asp Asp Thr Ala Met Tyr Phe Cys His Gln Ser Lys
 85 90 95

Lys Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Leu
 115 120 125

Glu Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr Val Thr Ile
 130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Lys Phe Gly Met Asn Trp
 145 150 155 160

Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met Gly Trp Ile His

165

170

175

Thr Ser Thr Gly Glu Pro Thr Tyr Ser Asp Asp Phe Lys Gly Arg Phe
 180 185 190

Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr Leu Arg Ile Asn
 195 200 205

Asn Leu Lys Asn Glu Asp Met Ala Lys Tyr Phe Cys Ala Arg Gly Gly
 210 215 220

Pro Tyr Val Arg Gly Ala Leu Asp Tyr Trp Gly Gln Gly Thr Ser Val
 225 230 235 240

Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Val Gln Ser
 245 250 255

Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
 260 265 270

Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln
 275 280 285

Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg
 290 295 300

Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr
 305 310 315 320

Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg
 325 330 335

Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His
 340 345 350

Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 355 360 365

Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
 370 375 380

Ala Asp Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser
 385 390 395 400

Pro Gly Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser
 405 410 415

Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp
 420 425 430

Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser
 435 440 445

Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu
 450 455 460

Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro
 465 470 475 480

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 485 490

<210> 217

<211> 1473

<212> DNA

<213> artificial sequence

<220>

<223> CD20xanti-CD3 VH5VL1

<400> 217

caaattgttc tctcccagtc tccagcaatc ctttctgcat ctccagggga gaaggtcaca	60
atgacttgca gggccagctc aagtttaagt ttcattgact ggtaccagca gaagccagga	120
tcctccccc aacctggat ttatgccaca tccaacctgg cttctggagt ccctgctcgc	180
ttcagtggca gtgggtctgg gacctcttac tctctcaca tcagcagagt ggaggctgaa	240
gatgctgcc cttatttctg ccatcagtgg agtagtaacc cgctcacgtt cgggtgctggg	300
acaaagggtg aaataaaagg tgggtggtgt tctggcggcg gcggctccgg tgggtggtgt	360
tctcaggtgc aactgcggca gcctggggct gagctggtga agcctggggc ctgagtgaag	420
atgtcctgca aggcttctgg ctacacattt accagttaca atatgcactg ggtaaagcag	480
acacctggac agggcctgga atggattgga gctatttata caggaaatgg tgatacttcc	540
tacaatcaga agttcaaagg caaggccaca ttgactgcag acaaatcctc cagcacagcc	600
tacatgcagc tcagcagtct gacatctgag gactctgcgg tctattactg tgcaagatcg	660
cactacggta gtaactacgt agactacttt gactactggg gccaaaggcac actagtcaca	720
gtctcgacag gaggtggtgg atccgacgtc caactggtgc agtcaggggc tgaagtgaaa	780

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aaacctgggg cctcagtga ggtgtcctgc aaggcttctg gctacacctt tactaggtac      840
acgatgcact gggtaaggca ggcacctgga cagggctctgg aatggattgg atacattaat      900
cctagccgtg gttatactaa ttacgcagac agcgtcaagg gccgcttcac aatcactaca      960
gacaaatcca ccagcacagc ctacatggaa ctgagcagcc tgcgttctga ggacactgca     1020
acctattact gtgcaagata ttatgatgat cattactgcc ttgactactg gggccaaggc     1080
accacgggtca ccgtctcctc aggcgaaggt actagtactg gttctgggtg aagtggaggt     1140
tcaggtggag cagacgacat tcagatgacc cagtctccat ctagectgtc tgcatctgtc     1200
ggggaccgtg tcaccatcac ctgcagagcc agtcaaagtg taagttacat gaactggtac     1260
cagcagaagc cgggcaaggc acccaaaaga tggatttatg acacatccaa agtggcttct     1320
ggagtccctg ctgcgttcag tggcagtggg tctgggaccg actactctct cacaatcaac     1380
agcttggagg ctgaagatgc tgccacttat tactgccaac agtggagtag taaccgctc      1440
acgttcggtg gcgggaccaa ggtggagatc aaa                                  1473

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<210> 218

<211> 491

<212> PRT

<213> artificial sequence

<220>

<223> CD20xanti-CD3 VH5VL1

<400> 218

```

Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
1           5           10           15

```

```

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Leu Ser Phe Met
          20           25           30

```

```

His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
          35           40           45

```

```

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
          50           55           60

```

```

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
65           70           75           80

```

```

Asp Ala Ala Thr Tyr Phe Cys His Gln Trp Ser Ser Asn Pro Leu Thr
          85           90           95

```

Phe Gly Ala Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Arg Gln Pro
 115 120 125

Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys
 130 135 140

Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys Gln
 145 150 155 160

Thr Pro Gly Gln Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn
 165 170 175

Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr
 180 185 190

Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr
 195 200 205

Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ser His Tyr Gly Ser
 210 215 220

Asn Tyr Val Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
 225 230 235 240

Val Ser Thr Gly Gly Gly Gly Ser Asp Val Gln Leu Val Gln Ser Gly
 245 250 255

Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala
 260 265 270

Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala
 275 280 285

Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly
 290 295 300

Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Thr Thr
 305 310 315 320

Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser
 325 330 335

Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr
 340 345 350

Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
 355 360 365

Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala
 370 375 380

Asp Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 385 390 395 400

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr
 405 410 415

Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
 420 425 430

Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly
 435 440 445

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala
 450 455 460

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu
 465 470 475 480

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 485 490

<210> 219

<211> 1473

<212> DNA

<213> artificial sequence

<220>

<223> CD20xanti-CD3 VH5VL2

<400> 219

caaattgttc tctcccagtc tccagcaatc ctttctgcat ctccagggga gaaggtcaca 60

atgacttgca gggccagctc aagtttaagt ttcatgcact ggtaccagca gaagccagga 120

tcctcccca aacctggat ttatgccaca tccaacctgg cttctggagt cctgctcgc 180

ttcagtgga gtgggtctgg gacctcttac tctctcaca tcagcagagt ggaggctgaa 240

gatgctgcca cttatttctg ccatcagtg agtagtaacc cgctcacgtt cggtgctggg 300

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acaaaggtgg aaataaaagg tgggtggtggt tctggcgggc gcggtccgg tgggtggtggt 360
tctcaggtgc aactgcggca gcctggggct gagctggtga agcctggggc ctcagtgaag 420
atgtcctgca aggcttctgg ctacacattt accagttaca atatgcactg ggtaaagcag 480
acacctggac agggcctgga atggattgga gctatttatc caggaaatgg tgatacttcc 540
tacaatcaga agttcaaagg caaggccaca ttgactgcag acaaatectc cagcacagcc 600
tacatgcagc tcagcagtct gacatctgag gactctgcgg tctattactg tgcaagatcg 660
cactacggtg gtaactacgt agactacttt gactactggg gccaaaggcac actagtcaca 720
gtctcgacag gaggtggtgg atccgacgtc caactggtgc agtcaggggc tgaagtgaag 780
aaacctgggg cctcagtga ggtgtcctgc aaggcttctg gctacacctt tactaggtac 840
acgatgcact gggtaaggca ggcacctgga cagggtctgg aatggattgg atacattaat 900
cctagccgtg gttatactaa ttacgcagac agcgtcaagg gccgcttcac aatcactaca 960
gacaaatcca ccagcacagc ctacatggaa ctgagcagcc tgcgttctga ggacactgca 1020
acctattact gtgcaagata ttatgatgat cattactgcc ttgactactg gggccaaggc 1080
accacggtca ccgtctctc aggcgaaggt actagtactg gttctggtgg aagtggaggt 1140
tcaggtggag cagacgacat tgtactgacc cagtctccag caactctgtc tctgtctcca 1200
ggggagcgtg ccacctgag ctgcagagcc agtcaaagt taagttacat gaactggtac 1260
cagcagaagc cgggcaaggc acccaaaaaga tggatttatg acacatccaa agtggcttct 1320
ggagtccctg ctgcgttcag tggcagtggg tctgggaccg actactctct cacaatcaac 1380
agcttgaggg ctgaagatgc tgccacttat tactgccaac agtggagtag taaccgctc 1440
acgttcggtg gcgggaccaa ggtggagatc aaa 1473

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<210> 220

<211> 491

<212> PRT

<213> artificial sequence

<220>

<223> CD20xanti-CD3 VH5VL2

<400> 220

```

Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
1           5           10          15

```

```

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Leu Ser Phe Met
20           25           30

```

His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
 35 40 45

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Phe Cys His Gln Trp Ser Ser Asn Pro Leu Thr
 85 90 95

Phe Gly Ala Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Arg Gln Pro
 115 120 125

Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys
 130 135 140

Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys Gln
 145 150 155 160

Thr Pro Gly Gln Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn
 165 170 175

Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr
 180 185 190

Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr
 195 200 205

Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ser His Tyr Gly Ser
 210 215 220

Asn Tyr Val Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
 225 230 235 240

Val Ser Thr Gly Gly Gly Gly Ser Asp Val Gln Leu Val Gln Ser Gly
 245 250 255

Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala
 260 265 270

Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala
 275 280 285

Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly
 290 295 300

Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Thr Thr
 305 310 315 320

Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser
 325 330 335

Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr
 340 345 350

Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
 355 360 365

Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala
 370 375 380

Asp Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro
 385 390 395 400

Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr
 405 410 415

Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
 420 425 430

Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly
 435 440 445

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala
 450 455 460

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu
 465 470 475 480

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 485 490

<211> 1473
 <212> DNA
 <213> artificial sequence

<220>
 <223> CD20xanti-CD3 VH5VL3

<400> 221
 caaattgttc tctcccagtc tccagcaatc ctttctgcat ctccagggga gaaggtcaca 60
 atgacttgca gggccagctc aagtttaagt ttcattgact ggtaccagca gaagccagga 120
 tcctcccca aacctggat ttatgccaca tccaacctgg cttctggagt cctgctcgc 180
 ttcagtggca gtgggtctgg gacctttac tctctcaca tcagcagagt ggaggctgaa 240
 gatgctgcca cttatttctg ccatcagtgg agtagtaacc cgctcacgtt cgggtgctggg 300
 acaaaggtgg aaataaaagg tgggtggtgg tctggcggcg gcggctccgg tgggtggtgg 360
 tctcaggtgc aactgcggca gcctggggct gagctggtga agcctggggc ctcaagtgaag 420
 atgtcctgca aggcttctgg ctacacattt accagttaca atatgcactg ggtaaagcag 480
 acacctggac agggcctgga atggattgga gctatttatc caggaaatgg tgatacttcc 540
 tacaatcaga agttcaaagg caaggccaca ttgactgcag acaaatcctc cagcacagcc 600
 tacatgcagc tcagcagctc gacatctgag gactctgcgg tctattactg tgcaagatcg 660
 cactacggta gtaactacgt agactacttt gactactggg gccaaaggcac actagtcaca 720
 gtctcgacag gaggtggtgg atccgacgtc caactggtgc agtcaggggc tgaagtgaag 780
 aaactctggg cctcagtga ggtgtcctgc aaggcttctg gctacacctt tactaggtac 840
 acgatgcact gggtaaggca ggcacctgga cagggtctgg aatggattgg atacattaat 900
 cctagccgtg gttataactaa ttacgcagac agcgtcaagg gccgcttcac aatcactaca 960
 gacaaatcca ccagcacagc ctacatggaa ctgagcagcc tgcgttctga ggacactgca 1020
 acctattact gtgcaagata ttatgatgat cattactgcc ttgactactg gggccaaggc 1080
 accacggtca ccgtctcctc aggcgaaggc actagtactg gttctggtgg aagtggaggt 1140
 tcaggtggag cagacgacat tgtactgacc cagtctccag caactctgtc tctgtctcca 1200
 ggggagcgtg ccacctgac ctgcagagcc agttcaagtg taagttacat gaactggtac 1260
 cagcagaagc cgggcaaggc acccaaaaga tggatttatg acacatccaa agtggcttct 1320
 ggagtccctg ctgcgttcag tggcagtggt tctgggaccg actactctct cacaatcaac 1380
 agcttgaggc ctgaagatgc tgccacttat tactgccaac agtggagtag taaccgcgtc 1440
 acgttcggtg gcgggaccaa ggtggagatc aaa 1473

<210> 222
 <211> 491
 <212> PRT
 <213> artificial sequence

<220>
 <223> CD20xanti-CD3 VH5VL3

<400> 222

Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
 1 5 10 15

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Leu Ser Phe Met
 20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
 35 40 45

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Phe Cys His Gln Trp Ser Ser Asn Pro Leu Thr
 85 90 95

Phe Gly Ala Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Arg Gln Pro
 115 120 125

Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys
 130 135 140

Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys Gln
 145 150 155 160

Thr Pro Gly Gln Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn
 165 170 175

Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr
 180 185 190

Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr

195	200	205
Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ser His Tyr Gly Ser		
210	215	220
Asn Tyr Val Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr		
225	230	235 240
Val Ser Thr Gly Gly Gly Gly Ser Asp Val Gln Leu Val Gln Ser Gly		
	245	250 255
Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala		
	260	265 270
Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala		
	275	280 285
Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly		
	290	295 300
Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Thr Thr		
305	310	315 320
Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser		
	325	330 335
Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr		
	340	345 350
Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly		
	355	360 365
Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala		
	370	375 380
Asp Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro		
385	390	395 400
Gly Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr		
	405	410 415
Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile		
	420	425 430

Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly
 435 440 445

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala
 450 455 460

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu
 465 470 475 480

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 485 490

<210> 223
 <211> 1473
 <212> DNA
 <213> artificial sequence

<220>
 <223> CD20xanti-CD3 VH7VL1

<400> 223
 caaatgttgc tctccagtc tccagcaatc ctttctgcat ctccagggga gaaggtcaca 60
 atgacttgca gggccagctc aagtttaagt ttcattgact ggtaccagca gaagccagga 120
 tcctccccc aaccctggat ttatgccaca tccaacctgg cttctggagt ccctgctcgc 180
 ttcagtggca gtgggtctgg gacctcttac tctctcacia tcagcagagt ggaggctgaa 240
 gatgctgcca cttatttctg ccatcagtgg agtagtaacc cgctcacgtt cggtgctggg 300
 acaaaggtgg aaataaaagg tgggtggtgt tctggcgccg gcggctccgg tgggtggtgt 360
 tctcaggtgc aactgcggca gcctggggct gagctggtga agcctggggc ctcagtgaag 420
 atgtcctgca aggcttctgg ctacacattt accagttaca atatgactg ggtaaagcag 480
 acacctggac agggcctgga atggattgga gctatttata caggaaatgg tgatacttcc 540
 tacaatcaga agttcaaagg caaggccaca ttgactgcag acaaatactc cagcacagcc 600
 tacatgcagc tcagcagtct gacatctgag gactctgcgg tctattactg tgcaagatcg 660
 cactacggta gtaactacgt agactacttt gactactggg gccaaaggcac actagtcaca 720
 gtctcgacag gaggtggtgg atccgacgtc caactggtgc agtcaggggc tgaagtgaag 780
 aaacctgggg cctcagtga ggtgtcctgc aaggcttctg gctacacctt tactaggtac 840
 acgatgcact gggtaaggca ggcacctgga cagggtctgg aatggattgg atacattaat 900
 cctagccgtg gttataactaa ttacaatcag aagttcaagg accgcgtcac aatcactaca 960
 gacaaatcca ccagcacagc ctacatggaa ctgagcagcc tgcgttctga ggacactgca 1020

gtctattact gtgcaagata ttatgatgat cattactgcc ttgactactg gggccaaggc 1080
 accacgggtca ccgtctcctc aggccaaggt actagtactg gttctgggtg aagtggaggt 1140
 tcaggtggag cagacgacat tcagatgacc cagtctccat ctacgctgtc tgcattctgtc 1200
 ggggaccgtg tcaccatcac ctgcagagcc agtcaaagtg taagttacat gaactggtac 1260
 cagcagaagc cgggcaaggc acccaaaaaga tggatttatg acacatccaa agtggcttct 1320
 ggagtccctg ctgcgttcag tggcagtggtg tctgggaccg actactctct cacaatcaac 1380
 agcttggagg ctgaagatgc tgccacttat tactgccaac agtggagtag taaccgctc 1440
 acgttcggtg gcgggaccaa ggtggagatc aaa 1473

<210> 224

<211> 491

<212> PRT

<213> artificial sequence

<220>

<223> CD20xanti-CD3 VH7VL1

<400> 224

Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
 1 5 10 15

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Leu Ser Phe Met
 20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
 35 40 45

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Phe Cys His Gln Trp Ser Ser Asn Pro Leu Thr
 85 90 95

Phe Gly Ala Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Arg Gln Pro
 115 120 125

Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys
 130 135 140

Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys Gln
 145 150 155 160

Thr Pro Gly Gln Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn
 165 170 175

Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr
 180 185 190

Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr
 195 200 205

Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ser His Tyr Gly Ser
 210 215 220

Asn Tyr Val Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
 225 230 235 240

Val Ser Thr Gly Gly Gly Gly Ser Asp Val Gln Leu Val Gln Ser Gly
 245 250 255

Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala
 260 265 270

Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala
 275 280 285

Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly
 290 295 300

Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Thr
 305 310 315 320

Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser
 325 330 335

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr
 340 345 350

Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
 355 360 365

Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala
370 375 380

Asp Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
385 390 395 400

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr
405 410 415

Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
420 425 430

Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly
435 440 445

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala
450 455 460

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu
465 470 475 480

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
485 490

<210> 225
<211> 1473
<212> DNA
<213> artificial sequence

<220>
<223> CD20xanti-CD3 VH7VL2

<400> 225
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tcctccccc aaccctggat ttatgccaca tccaacctgg cttctggagt ccctgctcgc 180
ttcagtggca gtgggtctgg gacctcttac tctctcacia tcagcagagt ggaggctgaa 240
gatgctgcc cttatttctg ccatcagtgg agtagtaacc cgctcacgtt cggtgctggg 300
acaaagggtg aaataaaaagg tgggtgggtg tctggcggcg gcggctccgg tgggtgggtg 360
tctcaggtgc aactgcggca gcctggggct gagctggtga agcctggggc ctgagtgaag 420
atgtcctgca aggcttctgg ctaacacattt accagttaca atatgcactg ggtaaagcag 480
acacctggac agggcctgga atggattgga gctattttatc caggaaatgg tgatacttcc 540

tacaatcaga agttcaaagg caaggccaca ttgactgcag acaaatcctc cagcacagcc 600
 tacatgcagc tcagcagtct gacatctgag gactctgcgg tctattactg tgcaagatcg 660
 cactacggta gtaactacgt agactacttt gactactggg gccaaaggcac actagtcaca 720
 gtctcgacag gaggtggtgg atccgacgtc caactggtgc agtcaggggc tgaagtgaag 780
 aaacctgggg cctcagtga ggtgtcctgc aaggcttctg gctacacctt tactaggtac 840
 acgatgcact gggttaaggca ggcacctgga caggggtctgg aatggattgg atacattaat 900
 cctagccgtg gttataactaa ttacaatcag aagttcaagg accgcgtcac aatcactaca 960
 gacaaatcca ccagcacagc ctacatggaa ctgagcagcc tgcgttctga ggacactgca 1020
 gtctattact gtgcaagata ttatgatgat cattactgcc ttgactactg gggccaaggc 1080
 accacggtca ccgtctctc aggcgaaggt actagtactg gttctggtgg aagtggaggt 1140
 tcaggtggag cagacgacat tgtactgacc cagtctccag caactctgtc tctgtctcca 1200
 ggggagcgtg ccaccctgag ctgcagagcc agtcaaagtg taagttacat gaactggtac 1260
 cagcagaagc cgggcaaggc acccaaaaga tggatttatg acacatccaa agtggcttct 1320
 ggagtccttg ctgccttcag tggcagtggg tctgggaccg actactctct cacaatcaac 1380
 agcttgaggg ctgaagatgc tgccacttat tactgccaac agtggagtag taaccgctc 1440
 acgttcggtg gcgggaccaa ggtggagatc aaa 1473

<210> 226
 <211> 491
 <212> PRT
 <213> artificial sequence

<220>
 <223> CD20xanti-CD3 VH7VL2

<400> 226

Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
 1 5 10 15

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Leu Ser Phe Met
 20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
 35 40 45

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Phe Cys His Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Ala Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Arg Gln Pro
115 120 125

Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys
130 135 140

Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys Gln
145 150 155 160

Thr Pro Gly Gln Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn
165 170 175

Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr
180 185 190

Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr
195 200 205

Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ser His Tyr Gly Ser
210 215 220

Asn Tyr Val Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
225 230 235 240

Val Ser Thr Gly Gly Gly Gly Ser Asp Val Gln Leu Val Gln Ser Gly
245 250 255

Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala
260 265 270

Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala
275 280 285

Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly
290 295 300

Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Thr
305 310 315 320

Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser
325 330 335

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr
340 345 350

Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
355 360 365

Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala
370 375 380

Asp Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro
385 390 395 400

Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr
405 410 415

Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
420 425 430

Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly
435 440 445

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala
450 455 460

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu
465 470 475 480

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
485 490

<210> 227

<211> 1473

<212> DNA

<213> artificial sequence

<220>

<223> CD20xanti-CD3 VH7VL3

<400> 227

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caaattgttc tctcccagtc tccagcaatc ctttctgcat ctccaggga gaaggtcaca      60
atgacttgca gggccagctc aagtttaagt ttcatgcact ggtaccagca gaagccagga      120
tcctcccca aaccctggat ttatgccaca tccaacctgg cttctggagt ccctgctcgc      180
ttcagtggca gtgggtctgg gacctcttac tctctcacia tcagcagagt ggaggctgaa      240
gatgctgcca cttatttctg ccatcagtgg agtagtaacc cgctcacgtt cgggtgctggg      300
acaaaggtgg aaataaaagg tgggtgggtg tctggcggcg gcggctccgg tgggtgggtg      360
tctcaggtgc aactgcggca gcctggggct gagctggtga agcctggggc ctcagtgaag      420
atgtcctgca aggccttctg ctacacattt accagttaca atatgcactg ggtaaagcag      480
acacctggac agggcctgga atggattgga gctatttatc caggaaatgg tgatacttcc      540
tacaatcaga agttcaaagg caaggccaca ttgactgcag acaaatcctc cagcacagcc      600
tacatgcagc tcagcagctc gacatctgag gactctgcgg tctattactg tgcaagatcg      660
cactacggta gtaactacgt agactacttt gactactggg gccaaaggcac actagtcaca      720
gtctcgacag gaggtggtgg atccgacgtc caactggtgc agtcaggggc tgaagtgaaa      780
aaacctgggg cctcagtga ggtgtcctgc aaggcttctg gctacacctt tactaggtac      840
acgatgcact gggtaaggca ggcacctgga cagggtctgg aatggattgg atacattaat      900
cctagccgtg gttatactaa ttacaatcag aagttcaagg accgcgtcac aatcactaca      960
gacaaatcca ccagcacagc ctacatggaa ctgagcagcc tgcgttctga ggacactgca     1020
gtctattact gtgcaagata ttatgatgat cattactgcc ttgactactg gggccaaggc     1080
accacggtca ccgtctctc aggcgaagggt actagtactg gttctggtgg aagtggaggt     1140
tcaggtggag cagacgacat tgtactgacc cagtctccag caactctgtc tctgtctcca     1200
ggggagcgtg ccacctgac ctgcagagcc agttcaagtg taagttacat gaactggtac     1260
cagcagaagc cgggcaaggc acccaaaaga tggatttatg acacatcaa agtggcttct     1320
ggagtccctg ctgcgttcag tggcagtggg tctgggaccg actactctct cacaatcaac     1380
agcttggagg ctgaagatgc tgccacttat tactgccaac agtggagtag taaccgctc     1440
acgttcggtg gcgggaccaa ggtggagatc aaa                                  1473

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<210> 228

<211> 491

<212> PRT

<213> artificial sequence

<220>

<223> CD20xanti-CD3 VH7VL3

<400> 228

Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
 1 5 10 15

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Leu Ser Phe Met
 20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
 35 40 45

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Phe Cys His Gln Trp Ser Ser Asn Pro Leu Thr
 85 90 95

Phe Gly Ala Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Arg Gln Pro
 115 120 125

Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys
 130 135 140

Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys Gln
 145 150 155 160

Thr Pro Gly Gln Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn
 165 170 175

Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr
 180 185 190

Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr
 195 200 205

Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ser His Tyr Gly Ser
 210 215 220

Asn Tyr Val Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr

225		230		235		240
Val Ser Thr Gly	Gly Gly Gly Ser Asp	Val Gln Leu Val Gln Ser Gly				
	245	250		255		
Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala						
	260	265		270		
Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala						
	275	280		285		
Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly						
	290	295		300		
Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Thr						
	305	310		315		320
Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser						
	325	330		335		
Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr						
	340	345		350		
Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly						
	355	360		365		
Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala						
	370	375		380		
Asp Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro						
	385	390		395		400
Gly Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr						
	405	410		415		
Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile						
	420	425		430		
Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly						
	435	440		445		
Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala						
	450	455		460		

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu
465 470 475 480

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
485 490

<210> 229
<211> 25
<212> PRT
<213> artificial sequence

<220>
<223> non-deimmunized anti-CD3 Framework 1
<400> 229

Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Thr Ser
20 25

<210> 230
<211> 15
<212> PRT
<213> artificial sequence

<220>
<223> non-deimmunized anti-CD3 Framework 2
<400> 230

Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
1 5 10 15

<210> 231
<211> 32
<212> PRT
<213> artificial sequence

<220>
<223> non-deimmunized anti-CD3 Framework 3
<400> 231

Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln
1 5 10 15

Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 232

<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> non-deimmunized anti-CD3 Framework 4

<400> 232

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
1 5 10

<210> 233
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> Sequence motif

<400> 233

Ala Ser Gly Tyr Thr Phe
1 5

<210> 234
<211> 4
<212> PRT
<213> artificial sequence

<220>
<223> Sequence motif

<400> 234

Met Glu Leu Ser
1

<210> 235
<211> 5
<212> PRT
<213> artificial sequence

<220>
<223> Sequence motif

<400> 235

Ile Thr Thr Asp Lys
1 5

<210> 236
<211> 1488
<212> DNA
<213> artificial sequence

<220>

<223> 5-10xVH5VL1 LHHL

<400> 236

gagctcgtga tgacacagtc tccatcctcc ctgactgtga cagcaggaga gaaggtcact	60
atgagctgca agtccagtc gagtctgtta aacagtggaa atcaaaagaa ctacttgacc	120
tgggtaccagc agaaaccagg gcagcctcct aaactgttga tctactgggc atccactagg	180
gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc	240
atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat	300
ccgctcacgt tcggtgctgg gaccaagctt gagatcaaag gtggtggtgg ttctggcggc	360
ggcggctccg gtggtggtgg ttctgagggt cagctgctcg agcagtctgg agctgagctg	420
gtaaggcctg ggacttcagt gaagatatcc tgcaaggctt ctggatacgc cttcactaac	480
tactggctag gttgggtaaa gcagaggcct ggacatggac ttgagtggat tggagatatt	540
ttccctggaa gtggtaatat ccactacaat gagaagttca agggcaaagc cacactgact	600
gcagacaaat cttcgagcac agcctatatg cagctcagta gcctgacatt tgaggactct	660
gctgtctatt tctgtgcaag actgaggaac tgggacgagc ctatggacta ctggggccaa	720
gggaccacgg tcaccgtctc ctccggaggt ggtggatccg acgtccaact ggtgcagtca	780
ggggctgaag tgaaaaaacc tggggcctca gtgaagggtg cctgcaaggc ttctggctac	840
acctttacta ggtacacgat gcactgggta aggcaggcac ctggacaggg tctggaatgg	900
attggataca ttaatcctag ccgtgggttat actaattacg cagacagcgt caagggccgc	960
ttcacaatca ctacagacaa atccaccagc acagcctaca tggaactgag cagcctgcgt	1020
tctgaggaca ctgcaacctt ttactgtgca agatattatg atgacatta ctgccttgac	1080
tactggggcc aaggcaccac ggtcacctgc tcctcaggcg aaggtagtag tactggttct	1140
ggtggaagtg gaggttcagg tggagcagac gacattcaga tgaccagtc tccatctagc	1200
ctgtctgcat ctgtcgggga ccgtgtcacc atcacctgca gagccagtc aagtgtgaagt	1260
tacatgaact ggtaccagca gaagccgggc aaggcaccca aaagatggat ttatgacaca	1320
tccaaagtgg cttctggagt ccctgctcgc ttcagtggca gtgggtctgg gaccgactac	1380
tctctcacia tcaacagctt ggaggctgaa gatgctgcca cttattactg ccaacagtgg	1440
agtagtaacc cgctcacgtt cgggtggcggg accaagggtg agatcaaa	1488

<210> 237

<211> 496

<212> PRT

<213> artificial sequence

<220>

<223> 5-10xVH5VL1 LHHL

<400> 237

Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
100 105 110

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
130 135 140

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
145 150 155 160

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
165 170 175

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
180 185 190

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
195 200 205

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
 210 215 220

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
 225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Val Gln
 245 250 255

Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys
 260 265 270

Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His
 275 280 285

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile
 290 295 300

Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg
 305 310 315 320

Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu
 325 330 335

Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr
 340 345 350

Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val
 355 360 365

Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly
 370 375 380

Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
 385 390 395 400

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
 405 410 415

Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
 420 425 430

Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro
 435 440 445

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
 450 455 460

Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 465 470 475 480

Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 485 490 495

<210> 238

<211> 1491

<212> DNA

<213> artificial sequence

<220>

<223> 5-10xVH5VL1 HLHL

<400> 238

gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggcttgggac ttcagtgaag	60
atatacctgca aggcttctgg atacgccttc actaactact ggctagggttg ggtaaagcag	120
aggcctggac atggacttga gtggattgga gatattttcc ctggaagtgg taatatccac	180
tacaatgaga agttcaaggg caaagccaca ctgactgcag acaaattcttc gagcacagcc	240
tatatgcagc tcagtagcct gacatttgag gactctgctg tctatttctg tgcaagactg	300
aggaactggg acgagcctat ggactactgg ggccaaggga ccacggtcac cgtctcctca	360
ggtgggtggg gttctggcgg cggcggctcc ggtgggtggg gttctgagct cgtgatgaca	420
cagtctccat cctccctgac tgtgacagca ggagagaagg tcactatgag ctgcaagtcc	480
agtcagagtc tgtaaacag tggaaatcaa aagaactact tgacctggta ccagcagaaa	540
ccagggcagc ctctaaact gttgatctac tgggcatcca ctagggaatc tggggtcctc	600
gatcgcttca caggcagtgg atctggaaca gatttcactc tcaccatcag cagtgtgcag	660
gctgaagacc tggcagttta ttactgtcag aatgattata gttatccgct cacgttcggt	720
gctgggacca agcttgagat caaatccgga ggtgggtggat ccgacgtcca actggtgcag	780
tcaggggctg aagtgaaaaa acctggggcc tcagtgaagg tgcctgcaa ggcttctggc	840
tacaccttta ctaggtacac gatgcactgg gtaaggcagg cacctggaca ggtcttgaa	900
tggattggat acattaatcc tagccgtggg tataactaatt acgcagacag cgtcaagggc	960
cgcttcacaa tcactacaga caaatccacc agcacagcct acatggaact gagcagcctg	1020
cgttctgagg aactgcaac ctattactgt gcaagatatt atgatgatca ttactgcctt	1080
gactactggg gccaaaggcac cacggtcacc gtctcctcag gcgaaggtag tagtactggg	1140

tctggtggaa gtggagggttc aggtggagca gacgacattc agatgaccca gtctccatct 1200
 agcctgtctg catctgtcgg ggaccgtgtc accatcacct gcagagccag tcaaagtgtg 1260
 agttacatga actggtacca gcagaagccg ggcaaggcac caaaagatg gatttatgac 1320
 acatccaaag tggcttctgg agtccctgct cgcttcagtg gcagtgggtc tgggaccgac 1380
 tactctctca caatcaacag cttggaggct gaagatgctg ccacttatta ctgccaaacag 1440
 tggagtagta acccgctcac gttcggtggc gggaccaagg tggagatcaa a 1491

<210> 239

<211> 497

<212> PRT

<213> artificial sequence

<220>

<223> 5-10xVH5VL1 HLHL

<400> 239

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
 1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
 20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
 35 40 45

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
 50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
 65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
 85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
 130 135 140

Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser
145 150 155 160

Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp
165 170 175

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala
180 185 190

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
210 215 220

Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly
225 230 235 240

Ala Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Val
245 250 255

Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val
260 265 270

Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met
275 280 285

His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
290 295 300

Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly
305 310 315 320

Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu
325 330 335

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg
340 345 350

Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr
355 360 365

Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser
370 375 380

Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser Pro Ser
385 390 395 400

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
405 410 415

Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys
420 425 430

Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val
435 440 445

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr
450 455 460

Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
465 470 475 480

Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
485 490 495

Lys

<210> 240
<211> 1488
<212> DNA
<213> artificial sequence

<220>
<223> 5-10xVL1VH5 LHLH

<400> 240
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atgagctgca agtccagtca gagtctgtta aacagtggaa atcaaaagaa ctacttgacc 120
tggtaccagc agaaaccagg gcagcctcct aaactgttga tctactgggc atccactagg 180
gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc 240
atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300
ccgctcacgt tcgggtgctgg gaccaagctt gagatcaaag gtggtggtgg ttctggcggc 360
ggcggctccg gtggtggtgg ttctgaggtg cagctgctcg agcagtctgg agctgagctg 420
gtaaggcctg ggacttcagt gaagatatcc tgcaaggctt ctggatacgc cttcactaac 480

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tactggctag gttgggtaaa gcagaggcct ggacatggac ttgagtggat tggagatatt 540
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gcagacaaat cttcgagcac agcctatatg cagctcagta gcctgacatt tgaggactct 660
gctgtctatt tctgtgcaag actgaggaac tgggacgagc ctatggacta ctggggccaa 720
gggaccacgg tcaccgtctc ctccggaggt ggtggatccg acattcagat gaccagctct 780
ccatctagcc tgtctgcac tgtcggggac cgtgtcacca tcacctgcag agccagtcaa 840
agtgttaagtt acatgaactg gtaccagcag aagccgggca aggcacccaa aagatggatt 900
tatgacacat ccaaagtggc ttctggagtc cctgctcgtc tcagtggcag tgggtctggg 960
accgactact ctctcacaat caacagcttg gaggctgaag atgctgccac ttattactgc 1020
caacagtgga gtagtaaccc gctcacgttc ggtggcgagg ccaaggtgga gatcaaaggc 1080
gaaggtaacta gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacgtccaa 1140
ctggtgcagt caggggctga agtgaaaaaa cctggggcct cagtgaaggt gtcctgcaag 1200
gcttctggct acacctttac taggtacacg atgcactggg taaggcaggc acctggacag 1260
ggtctggaat ggattggata cattaatcct agccgtgggt atactaatta cgcagacagc 1320
gtcaagggcc gcttcacaat cactacagac aaatccacca gcacagccta catggaactg 1380
agcagcctgc gttctgagga cactgcaacc tattactgtg caagatatta tgatgatcat 1440
tactgccttg actactgggg ccaaggcacc acggtcaccg tctcctca 1488

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<210> 241

<211> 496

<212> PRT

<213> artificial sequence

<220>

<223> 5-10xVL1VH5 LHLH

<400> 241

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Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
1           5           10           15

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Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20           25           30

```

```

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35           40           45

```

```

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50           55           60

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Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80
 Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
 85 90 95
 Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
 100 105 110
 Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 115 120 125
 Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
 130 135 140
 Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
 145 150 155 160
 Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
 165 170 175
 Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
 180 185 190
 Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
 195 200 205
 Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
 210 215 220
 Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
 225 230 235 240
 Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Gln
 245 250 255
 Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
 260 265 270
 Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr
 275 280 285
 Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser

290

295

300

Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
305 310 315 320

Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala
325 330 335

Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly
340 345 350

Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly Ser Gly
355 360 365

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val Gln Ser
370 375 380

Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
385 390 395 400

Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln
405 410 415

Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg
420 425 430

Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Thr
435 440 445

Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg
450 455 460

Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His
465 470 475 480

Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
485 490 495

<210> 242

<211> 1491

<212> DNA

<213> artificial sequence

<220>

<223> 5-10xVL1VH5 HLLH

<400> 242

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atatacctgca aggcttctgg atacgccttc actaactact ggctagggtg ggtaaagcag 120
aggcctggac atggacttga gtggattgga gatattttcc ctggaagtgg taatatccac 180
tacaatgaga agttcaaggg caaagccaca ctgactgcag acaaatcttc gagcacagcc 240
tatatgcagc tcagtagcct gacatttgag gactctgctg tctatttctg tgcaagactg 300
aggaactggg acgagcctat ggactactgg ggccaagggg ccacggtcac cgtctcctca 360
ggtggtggtg gttctggcgg cggcggtcc ggtggtggtg gttctgagct cgtgatgaca 420
cagtctccat cctccctgac tgtgacagca ggagagaagg tcactatgag ctgcaagtcc 480
agtcagagtc tgttaaacag tggaaatcaa aagaactact tgacctggta ccagcagaaa 540
ccagggcagc ctctaaact gttgatctac tgggcatcca ctagggaatc tggggtcct 600
gatcgcttca caggcagtgg atctggaaca gatttcactc tcaccatcag cagtgtgcag 660
gctgaagacc tggcagttta ttactgtcag aatgattata gttatccgct cacgttcggt 720
gctgggacca agcttgagat caaatccgga ggtggtggat ccgacattca gatgaccag 780
tctccatcta gcctgtctgc atctgtcggg gaccgtgtca ccatcacctg cagagccagt 840
caaagtgtaa gttacatgaa ctgggtaccag cagaagccgg gcaaggcacc caaaagatgg 900
atztatgaca catccaaagt ggcttctgga gtccctgctc gtttcagtgg cagtgggtct 960
gggaccgact actctctcac aatcaacagc ttggaggctg aagatgctgc cacttattac 1020
tgccaacagt ggagtagtaa cccgctcacg ttcggtggcg ggaccaaggt ggagatcaaa 1080
ggcgaaggta ctagtactgg ttctggtgga agtggaggtt caggtggagc agacgacgct 1140
caactggtgc agtcaggggc tgaagtgaaa aaacctgggg cctcagtga ggtgtcctgc 1200
aaggcttctg gctacacctt tactaggtac acgatgcact gggttaaggca ggcacctgga 1260
cagggctctg aatggattgg atacattaat cctagccgtg gttatactaa ttacgcagac 1320
agcgtcaagg gccgcttcac aatcactaca gacaaatcca ccagcacagc ctacatggaa 1380
ctgagcagcc tgcgttctga ggacactgca acctattact gtgcaagata ttatgatgat 1440
cattactgcc ttgactactg gggccaaggc accacggtca ccgtctctc a 1491

<210> 243

<211> 497

<212> PRT

<213> artificial sequence

<220>

<223> 5-10xVL1VH5 HLLH

<400> 243

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
 1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
 20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
 35 40 45

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
 50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
 65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
 85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
 130 135 140

Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser
 145 150 155 160

Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp
 165 170 175

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala
 180 185 190

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
 195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
 210 215 220

Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly
 225 230 235 240

Ala Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Ile
 245 250 255

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 260 265 270

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp
 275 280 285

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr
 290 295 300

Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
 305 310 315 320

Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala
 325 330 335

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly
 340 345 350

Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly Ser
 355 360 365

Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val Gln
 370 375 380

Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys
 385 390 395 400

Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg
 405 410 415

Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser
 420 425 430

Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile
 435 440 445

Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu
 450 455 460

Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp
 465 470 475 480

His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 485 490 495

Ser

<210> 244
 <211> 1491
 <212> DNA
 <213> artificial sequence

<220>
 <223> 5-10xVH5VL2 HLHL

<400> 244
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 aggctgggac atggacttga gtggattgga gatattttcc ctggaagtgg taatatccac 180
 tacaatgaga agttcaaggg caaagccaca ctgactgcag acaaattcttc gagcacagcc 240
 tatatgcagc tcagtagcct gacatttgag gactctgctg tctattttctg tgcaagactg 300
 aggaactggg acgagcctat ggactactgg ggccaaggga ccacggtcac cgtctcctca 360
 ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctgagct cgtgatgaca 420
 cagtctccat cctccctgac tgtgacagca ggagagaagg tcaactatgag ctgcaagtcc 480
 agtcagagtc tgtaaacag tggaaatcaa aagaactact tgacctggta ccagcagaaa 540
 ccagggcagc ctctaaact gttgatctac tgggcatcca ctagggaatc tggggtcctt 600
 gatcgcttca caggcagtggt atctggaaca gatttcactc tcaccatcag cagtgtgcag 660
 gctgaagacc tggcagttta ttactgtcag aatgattata gttatccgct cacgttcggt 720
 gctgggacca agcttgagat caaatccgga ggtggtggat ccgacgtcca actggtgcag 780
 tcaggggctg aagtgaaaaa acctggggcc tcagtgaagg tgtcctgcaa ggcttctggc 840
 tacaccttta ctaggtacac gatgcactgg gtaaggcagg cacctggaca gggctctggaa 900
 tggattggat acattaatcc tagccgtggt tatactaatt acgcagacag cgtcaagggc 960
 cgcttcacaa tcactacaga caaatccacc agcacagcct acatggaact gagcagcctg 1020
 cgttctgagg aactgcaac ctattactgt gcaagatatt atgatgatca ttactgcctt 1080
 gactactggg gccaaaggcac cacggtcacc gtctcctcag gcgaaggtag tagtactggt 1140

tctggtggaa gtggaggttc aggtggagca gacgacattg tactgaccca gtctccagca 1200
 actctgtctc tgtctccagg ggagcgtgcc accctgagct gcagagccag tcaaagtgtg 1260
 agttacatga actggtacca gcagaagccg ggcaaggcac ccaaagatg gatttatgac 1320
 acatccaaag tggcttctgg agtccctgct cgcttcagtg gcagtgggtc tgggaccgac 1380
 tactctctca caatcaacag cttggaggct gaagatgctg ccacttatta ctgccaacag 1440
 tggagtagta acccgctcac gttcgggtggc gggaccaagg tggagatcaa a 1491

<210> 245

<211> 497

<212> PRT

<213> artificial sequence

<220>

<223> 5-10xVH5VL2 HLHL

<400> 245

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
 1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
 20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
 35 40 45

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
 50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
 65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
 85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
 130 135 140

Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser
 145 150 155 160

Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp
 165 170 175

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala
 180 185 190

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
 195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
 210 215 220

Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly
 225 230 235 240

Ala Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Val
 245 250 255

Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val
 260 265 270

Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met
 275 280 285

His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
 290 295 300

Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly
 305 310 315 320

Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu
 325 330 335

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg
 340 345 350

Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr
 355 360 365

Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser
 370 375 380

Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro Ala
385 390 395 400

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
405 410 415

Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys
420 425 430

Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val
435 440 445

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr
450 455 460

Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
465 470 475 480

Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
485 490 495

Lys

<210> 246
<211> 1488
<212> DNA
<213> artificial sequence

<220>
<223> 5-10xVL2VH5 LHLH

<400> 246
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tggtaccagc agaaaccagg gcagcctcct aaactgttga tctactgggc atccactagg 180
gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc 240
atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300
ccgctcacgt tcggtgctgg gaccaagctt gagatcaaag gtggtggtgg ttctggcggc 360
ggcggtccg gtggtggtgg ttctgaggtg cagctgctcg agcagtctgg agctgagctg 420
gtaaggcctg ggacttcagt gaagatatcc tgcaaggctt ctggatacgc cttcactaac 480

tactggctag gttgggtaaa gcagaggcct ggacatggac ttgagtggat tggagatatt 540
 ttccctggaa gtggtaatat ccactacaat gagaagttca agggcaaagc cacactgact 600
 gcagacaaat cttcgagcac agcctatatg cagctcagta gcctgacatt tgaggactct 660
 gctgtctatt tctgtgcaag actgaggaac tgggacgagc ctatggacta ctggggccaa 720
 gggaccacgg tcaccgtctc ctccggaggt ggtggatccg acattgtact gaccagtct 780
 ccagcaactc tgtctctgtc tccaggggag cgtgccacc tgagctgcag agccagtcaa 840
 agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcacccaa aagatggatt 900
 tatgacacat ccaaagtggc ttctggagtc cctgctcgtc tcagtggcag tgggtctggg 960
 accgactact ctctcacaat caacagcttg gaggtgaag atgctgccac ttattactgc 1020
 caacagtgga gtagtaaccc gctcacgttc ggtggcgagg ccaaggtgga gatcaaaggc 1080
 gaaggacta gtactggttc tgggtggaagt ggaggttcag gtggagcaga cgacgtccaa 1140
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 gtcaagggcc gttcacaat cactacagac aaatccacca gcacagccta catggaactg 1380
 agcagcctgc gttctgagga cactgcaacc tattactgtg caagatatta tgatgatcat 1440
 tactgccttg actactgggg ccaaggcacc acggtcaccg tctcctca 1488

<210> 247

<211> 496

<212> PRT

<213> artificial sequence

<220>

<223> 5-10xVL2VH5 LHLH

<400> 247

Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
 1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
 20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
100 105 110

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
130 135 140

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
145 150 155 160

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
165 170 175

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
180 185 190

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
195 200 205

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
210 215 220

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Val
245 250 255

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
260 265 270

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr
275 280 285

Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser

290

295

300

Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
 305 310 315 320

Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala
 325 330 335

Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly
 340 345 350

Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly Ser Gly
 355 360 365

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val Gln Ser
 370 375 380

Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
 385 390 395 400

Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln
 405 410 415

Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg
 420 425 430

Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Thr
 435 440 445

Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg
 450 455 460

Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His
 465 470 475 480

Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 485 490 495

<210> 248

<211> 1491

<212> DNA

<213> artificial sequence

<220>

<223> 5-10xVL2VH5 HLLH

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<400> 248
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aggcctggac atggacttga gtggattgga gatattttcc ctggaagtgg taatatccac      180
tacaatgaga agttcaaggg caaagccaca ctgactgcag acaaatcttc gagcacagcc      240
tatatgcagc tcagtagcct gacatttgag gactctgctg tctatttctg tgcaagactg      300
aggaactggg acgagcctat ggactactgg ggccaaggga ccacggtcac cgtctcctca      360
ggtggtggtg gttctggcgg cggcggtccc ggtggtggtg gttctgagct cgtgatgaca      420
cagtctccat cctccctgac tgtgacagca ggagagaagg tcactatgag ctgcaagtcc      480
agtcagagtc tgttaaacag tggaaatcaa aagaactact tgacctggtg ccagcagaaa      540
ccagggcagc ctctaaact gttgatctac tgggcatcca ctagggaatc tggggtcctt      600
gatcgcttca caggcagtgg atctggaaca gatttcactc tcaccatcag cagtgtgcag      660
gctgaagacc tggcagttta ttactgtcag aatgattata gttatccgct cacgttcggt      720
gctgggacca agcttgagat caaatccgga ggtggtggat ccgacattgt actgaccag      780
tctccagcaa ctctgtctct gtctccaggg gagcgtgcca ccctgagctg cagagccagt      840
caaagtgtaa gttacatgaa ctggtaccag cagaagccgg gcaaggcacc caaaagatgg      900
atttatgaca catccaaagt ggcttctgga gtccctgctc gtttcagtgg cagtgggtct      960
gggaccgact actctctcac aatcaacagc ttggaggctg aagatgctgc cacttattac     1020
tgccaacagt ggagtagtaa cccgctcagc ttcggtggcg ggaccaaggt ggagatcaaa     1080
ggcgaaggta ctagtactgg ttctggtgga agtggaggtt caggtggagc agacgacgtc     1140
caactggtgc agtcaggggc tgaagtgaaa aaacctgggg cctcagtga ggtgtcctgc     1200
aaggcttctg gctacacctt tactaggtac acgatgcact gggttaaggca ggcacctgga     1260
cagggctctg aatggattgg atacattaat cctagccgtg gttatactaa ttacgcagac     1320
agcgtcaagg gccgcttcac aatcactaca gacaaatcca ccagcacagc ctacatggaa     1380
ctgagcagcc tgcgttctga ggacactgca acctattact gtgcaagata ttatgatgat     1440
cattactgcc ttgactactg gggccaaggc accacggtca ccgtctctc a                 1491

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<210> 249

<211> 497

<212> PRT

<213> artificial sequence

<220>

<223> 5-10xVL2VH5 HLLH

<400> 249

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
 1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
 20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
 35 40 45

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
 50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
 65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
 85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
 130 135 140

Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser
 145 150 155 160

Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp
 165 170 175

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala
 180 185 190

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
 195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
 210 215 220

Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly
225 230 235 240

Ala Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Ile
245 250 255

Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg
260 265 270

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp
275 280 285

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr
290 295 300

Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
305 310 315 320

Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala
325 330 335

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly
340 345 350

Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly Ser
355 360 365

Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val Gln
370 375 380

Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys
385 390 395 400

Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg
405 410 415

Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser
420 425 430

Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile
435 440 445

Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu
450 455 460

Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp
 465 470 475 480

His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 485 490 495

Ser

<210> 250
 <211> 1488
 <212> DNA
 <213> artificial sequence

<220>
 <223> 5-10 VH5VL3 LHHL

<400> 250
 gagctcgtga tgacacagtc tccatcctcc ctgactgtga cagcaggaga gaaggtcact 60
 atgagctgca agtccagtcā gagtctgtta aacagtggaa atcaaaagaa ctacttgacc 120
 tgggtaccagc agaaaccagg gcagcctcct aaactgttga tctactgggc atccactagg 180
 gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc 240
 atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300
 ccgctcacgt tcgggtgctgg gaccaagctt gagatcaaag gtgggtggtgg ttctggcggc 360
 ggoggctccg gtgggtggtgg ttctgaggtg cagctgctcg agcagtctgg agctgagctg 420
 gtaaggcctg ggacttcagt gaagatatcc tgcaaggctt ctggatacgc cttcactaac 480
 tactggctag gttgggtaaa gcagaggcct ggacatggac ttgagtggat tggagatatt 540
 ttccctggaa gtggtaatat cactacaat gagaagttca agggcaaagc cacactgact 600
 gcagacaaat cttcgagcac agcctatatg cagctcagta gcctgacatt tgaggactct 660
 gctgtctatt tctgtgcaag actgaggaac tgggacgagc ctatggacta ctggggccaa 720
 gggaccacgg tcaccgtctc ctccggaggt ggtggatccg acgtccaact ggtgcagtca 780
 ggggctgaag tgaaaaaacc tggggcctca gtgaagggtg cctgcaaggc ttctggctac 840
 acctttacta ggtacacgat gcactgggta aggcaggcac ctggacaggg tctggaatgg 900
 attggataca ttaatcctag ccgtgggtat actaattacg cagacagcgt caagggccgc 960
 ttcacaatca ctacagacaa atccaccagc acagcctaca tggaactgag cagcctgcgt 1020
 tctgaggaca ctgcaaccta ttactgtgca agatattatg atgacatta ctgccttgac 1080
 tactggggcc aaggcaccac ggtcacgcgc tcctcaggcg aaggtagtag tactggttct 1140

ggtggaagtg gaggttcagg tggagcagac gacattgtac tgaccagtc tccagcaact 1200
 ctgtctctgt ctccagggga gcgtgccacc ctgacctgca gagccagttc aagtgttaagt 1260
 tacatgaact ggtaccagca gaagccgggc aaggcaccca aaagatggat ttatgacaca 1320
 tccaaagtgg cttctggagt ccctgctcgc ttcagtggca gtgggtctgg gaccgactac 1380
 tctctcaciaa tcaacagctt ggaggctgaa gatgctgcca cttattactg ccaacagtgg 1440
 agtagtaacc cgctcacgtt cggtggcggg accaaggtgg agatcaaa 1488

<210> 251

<211> 496

<212> PRT

<213> artificial sequence

<220>

<223> 5-10VH5VL3 LHHL

<400> 251

Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
 1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
 20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
 85 90 95

Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
 100 105 110

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 115 120 125

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
 130 135 140

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
145 150 155 160

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
165 170 175

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
180 185 190

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
195 200 205

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
210 215 220

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Val Gln
245 250 255

Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys
260 265 270

Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His
275 280 285

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile
290 295 300

Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg
305 310 315 320

Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu
325 330 335

Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr
340 345 350

Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val
355 360 365

Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly
370 375 380

Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro Ala Thr
385 390 395 400

Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser
405 410 415

Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
420 425 430

Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro
435 440 445

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
450 455 460

Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
465 470 475 480

Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
485 490 495

<210> 252

<211> 1491

<212> DNA

<213> artificial sequence

<220>

<223> 5-10VH5VL3 HLHL

<400> 252

gagggtgcagc tgctcgagca gtctggagct gagctggtaa ggcctgggac ttcagtgaag 60

atatacctgca aggcttctgg atacgccttc actaactact ggctagggtg ggtaaagcag 120

aggcctggac atggacttga gtggattgga gatattttcc ctggaagtgg taatatccac 180

tacaatgaga agttcaaggg caaagccaca ctgactgcag acaaattctc gagcacagcc 240

tatatgcagc tcagtagcct gacatttgag gactctgctg tctattttctg tgcaagactg 300

aggaactggg acgagcctat ggactactgg ggccaaggga ccacggtcac cgtctcctca 360

ggtgggtggtg gttctggcgg cggcggctcc ggtgggtggtg gttctgagct cgtgatgaca 420

cagtctccat cctccctgac tgtgacagca ggagagaagg tcaactatgag ctgcaagtcc 480

agtcagagtc tgtaaacag tggaaatcaa aagaactact tgacctggta ccagcagaaa 540

ccagggcagc ctctaaact gttgatctac tgggcatcca ctagggaatc tggggtcct 600

gatcgcttca caggcagtgg atctggaaca gatttcactc tcaccatcag cagtgtgcag 660
gctgaagacc tggcagttta ttactgtcag aatgattata gttatccgct cacgttcggt 720
gctgggacca agcttgagat caaatccgga ggtggtggat ccgacgtcca actggtgcag 780
tcaggggctg aagtgaaaaa acctggggcc tcagtgaagg tgtcctgcaa ggcttctggc 840
tacaccttta ctaggtacac gatgcactgg gtaaggcagg cacctggaca gggctctggaa 900
tggattggat acattaatcc tagccgtggt tatactaatt acgcagacag cgtcaagggc 960
cgcttcacaa tctactacaga caaatccacc agcacagcct acatggaact gagcagcctg 1020
cgttctgagg aactgcaac ctattactgt gcaagatatt atgatgatca ttactgcctt 1080
gactactggg gccaaaggcac caccgtcacc gtctcctcag gcgaaggtag tagtactggt 1140
tctgggtggaa gtggagggttc aggtggagca gacgacattg tactgaccca gtctccagca 1200
actctgtctc tgtctccagg ggagcgtgcc accctgacct gcagagccag ttcaagtgt 1260
agttacatga actggtacca gcagaagccg ggcaaggcac ccaaaagatg gatttatgac 1320
acatccaaag tggcttctgg agtccttctg cgcttcagtg gcagtgggtc tgggaccgac 1380
tactctctca caatcaacag cttggaggct gaagatgctg ccacttatta ctgccaacag 1440
tggagtagta acccgctcac gttcggtggc gggaccaagg tggagatcaa a 1491

<210> 253

<211> 497

<212> PRT

<213> artificial sequence

<220>

<223> 5-10VH5VL3 HLHL

<400> 253

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35 40 45

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
130 135 140

Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser
145 150 155 160

Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp
165 170 175

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala
180 185 190

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
210 215 220

Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly
225 230 235 240

Ala Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Val
245 250 255

Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val
260 265 270

Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met
275 280 285

His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
290 295 300

Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly

305 310 315 320
 Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu
 325 330 335
 Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg
 340 345 350
 Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr
 355 360 365
 Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser
 370 375 380
 Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro Ala
 385 390 395 400
 Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys Arg Ala
 405 410 415
 Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys
 420 425 430
 Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val
 435 440 445
 Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr
 450 455 460
 Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
 465 470 475 480
 Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
 485 490 495

Lys

<210> 254
 <211> 1488
 <212> DNA
 <213> artificial sequence

<220>
 <223> 5-10VL3VH5 LHLH

<400> 254
 gagctcgtga tgacacagtc tccatcctcc ctgactgtga cagcaggaga gaaggctcact 60
 atgagctgca agtccagtca gagtctgtta aacagtggaa atcaaaagaa ctacttgacc 120
 tgggtaccagc agaaaccagg gcagcctcct aaactgttga tctactgggc atccactagg 180
 gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc 240
 atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300
 ccgctcacgt tcggtgctgg gaccaagctt gagatcaaag gtggtggtgg ttctggcggc 360
 ggcggctccg gtggtggtgg ttctgaggtg cagctgctcg agcagtctgg agctgagctg 420
 gtaaggcctg ggacttcagt gaagatatcc tgcaaggctt ctggatacgc cttcactaac 480
 tactggctag gttgggtaaa gcagaggcct ggacatggac ttgagtggat tggagatatt 540
 ttccctggaa gtggtaatat ccactacaat gagaagttca agggcaaagc cacactgact 600
 gcagacaaat cttcgagcac agcctatatg cagctcagta gcctgacatt tgaggactct 660
 gctgtctatt tctgtgcaag actgaggaac tgggacgagc ctatggacta ctggggccaa 720
 gggaccacgg tcaccgtctc ctccggaggt ggtggatccg acattgtact gacccagtct 780
 ccagcaactc tgtctctgtc tccaggggag cgtgccaccc tgacctgcag agccagttca 840
 agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcacccaa aagatggatt 900
 tatgacacat ccaaagtggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg 960
 accgactact ctctcacaat caacagcttg gaggtgaag atgctgccac ttattactgc 1020
 caacagtgga gtagtaaccc gctcacgttc ggtggcggga ccaaggtgga gatcaaaggc 1080
 gaaggctacta gtactggttc tgggtggaagt ggaggttcag gtggagcaga cgacgtccaa 1140
 ctggtgcagt caggggctga agtgaaaaaa cctggggcct cagtgaaggt gtccctgcaag 1200
 gcttctggct acacctttac taggtacacg atgcactggg taaggcaggc acctggacag 1260
 ggtctggaat ggattggata cattaatcct agccgtgggt atactaatta cgcagacagc 1320
 gtcaagggcc gcttcacaat cactacagac aaatccacca gcacagccta catggaactg 1380
 agcagcctgc gttctgagga cactgcaacc tattactgtg caagatatta tgatgatcat 1440
 tactgccttg actactgggg ccaaggcacc acggtcaccg tctcctca 1488

<210> 255

<211> 496

<212> PRT

<213> artificial sequence

<220>

<223> 5-10VL3VH5 LHLH

<400> 255

Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
100 105 110

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
130 135 140

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
145 150 155 160

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
165 170 175

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
180 185 190

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
195 200 205

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
210 215 220

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
 225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Val
 245 250 255

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
 260 265 270

Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr
 275 280 285

Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser
 290 295 300

Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
 305 310 315 320

Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala
 325 330 335

Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly
 340 345 350

Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly Ser Gly
 355 360 365

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val Gln Ser
 370 375 380

Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
 385 390 395 400

Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln
 405 410 415

Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg
 420 425 430

Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Thr
 435 440 445

Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg
 450 455 460

Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His
 465 470 475 480

Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 485 490 495

<210> 256
 <211> 1491
 <212> DNA
 <213> artificial sequence

<220>
 <223> 5-10VL3VH5 HLLH

<400> 256
 gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggctgggac ttcagtgaag 60
 atatcctgca aggcttctgg atacgccttc actaactact ggctaggttg ggtaaagcag 120
 aggctggac atggacttga gtggattgga gatattttcc ctggaagtgg taatatccac 180
 tacaatgaga agttcaaggg caaagccaca ctgactgcag acaaactctc gagcacagcc 240
 tatatgcagc tcagtagcct gacatttgag gactctgctg tctatttctg tgcaagactg 300
 aggaactggg acgagcctat ggactactgg ggccaaggga ccacggtcac cgtctcctca 360
 ggtggtggtg gttctggcgg cggcggtcc ggtggtggtg gttctgagct cgtgatgaca 420
 cagtctccat cctccctgac tgtgacagca ggagagaagg tcactatgag ctgcaagtcc 480
 agtcagagtc tgtaaacag tggaatcaa aagaactact tgacctggtt ccagcagaaa 540
 ccagggcagc ctctaaact gttgatctac tgggcatcca ctagggaatc tggggctcct 600
 gatcgcttca caggcagtgg atctggaaca gatttctctc tcaccatcag cagtgtgcag 660
 gctgaagacc tggcagttta ttactgtcag aatgattata gttatccgct cacgttcggt 720
 gctgggacca agcttgagat caaatccgga ggtggtggat ccgacattgt actgaccag 780
 tctccagcaa ctctgtctct gtctccaggg gagcgtgcca cctgacctg cagagccagt 840
 tcaagtgtaa gttacatgaa ctggtaccag cagaagccgg gcaaggcacc caaaagatgg 900
 atttatgaca catccaaagt ggcttctgga gtccctgctc gcttcagtgg cagtgggtct 960
 gggaccgact actctctcac aatcaacagc ttggaggctg aagatgctgc cacttattac 1020
 tgccaacagt ggagtagtaa cccgctcacg ttcgggtggc ggaccaaggt ggagatcaaa 1080
 ggcgaaggta ctagtactgg ttctggtgga agtggaggtt caggtggagc agacgacgtc 1140
 caactggtgc agtcaggggc tgaagtgaaa aaacctgggg cctcagtga ggtgtcctgc 1200
 aaggcttctg gctacacctt tactaggtac acgatgcact gggttaaggca ggcacctgga 1260

cagggtctgg aatggattgg atacattaat cctagccgtg gttataactaa ttacgcagac 1320
 agcgtcaagg gccgcttcac aatcactaca gacaaatcca ccagcacagc ctacatggaa 1380
 ctgagcagcc tgcgttctga ggacactgca acctattact gtgcaagata ttatgatgat 1440
 cattactgcc ttgactactg gggccaaggc accacggtca ccgtctctc a 1491

<210> 257

<211> 497

<212> PRT

<213> artificial sequence

<220>

<223> 5-10VL3VH5 HLLH

<400> 257

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
 1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
 20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
 35 40 45

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
 50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
 65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
 85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
 130 135 140

Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser
 145 150 155 160

Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp
 165 170 175

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala
 180 185 190

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
 195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
 210 215 220

Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly
 225 230 235 240

Ala Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Ile
 245 250 255

Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg
 260 265 270

Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
 275 280 285

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr
 290 295 300

Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Ser Gly Ser
 305 310 315 320

Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala
 325 330 335

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly
 340 345 350

Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly Ser
 355 360 365

Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val Gln
 370 375 380

Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys
 385 390 395 400

Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg
 405 410 415

Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser
 420 425 430

Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile
 435 440 445

Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu
 450 455 460

Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp
 465 470 475 480

His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 485 490 495

Ser

<210> 258
 <211> 1488
 <212> DNA
 <213> artificial sequence

<220>
 <223> 5-10VH7VL1 LHHL

<400> 258
 gagctcgtga tgacacagtc tccatcctcc ctgactgtga cagcaggaga gaaggtcact 60
 atgagctgca agtccagtca gagtctgtta aacagtggaa atcaaaagaa ctacttgacc 120
 tgggtaccagc agaaaccagg gcagcctcct aaactgttga tctactgggc atccactagg 180
 gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc 240
 atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300
 ccgctcacgt tcggtgctgg gaccaagctt gagatcaaag gtggtggtgg ttctggcggc 360
 ggcgggtccg gtggtggtgg ttctgaggtg cagctgctcg agcagtctgg agctgagctg 420
 gtaaggcctg ggacttcagt gaagatatcc tgcaaggctt ctggatacgc cttcactaac 480
 tactggctag gttgggtaaa gcagaggcct ggacatggac ttgagtggat tggagatatt 540
 ttccctggaa gtggtaatat cactacaat gagaagttca agggcaaagc cacactgact 600

gcagacaaat cttcgagcac agcctatatg cagctcagta gcctgacatt tgaggactct 660
 gctgtctatt tctgtgcaag actgaggaac tgggacgagc ctatggacta ctggggccaa 720
 gggaccacgg tcaccgtctc ctccggaggt ggtggatccg acgtccaact ggtgcagtca 780
 ggggctgaag tgaaaaaacc tggggcctca gtgaaggtgt cctgcaaggc ttctggctac 840
 acctttacta ggtacacgat gcactgggta aggcaggcac ctggacaggg tctggaatgg 900
 attggataca ttaatcctag ccgtgggttat actaattaca atcagaagtt caaggaccgc 960
 gtcacaatca ctacagacaa atccaccagc acagcctaca tggaactgag cagcctgcgt 1020
 tctgaggaca ctgcagtcta ttactgtgca agatattatg atgataatta ctgccttgac 1080
 tactggggcc aaggcaccac ggtcaccgtc tcctcaggcg aaggtactag tactggttct 1140
 ggtggaagtg gaggttcagg tggagcagac gacattcaga tgaccagtc tccatctagc 1200
 ctgtctgcat ctgtcgggga ccgtgtcacc atcacctgca gagccagtca aagtgttaagt 1260
 tacatgaact ggtaccagca gaagccgggc aaggcaccca aaagatggat ttatgacaca 1320
 tccaaagtgg cttctggagt ccctgctcgc ttcagtggca gtgggtctgg gaccgactac 1380
 tctctcacia tcaacagctt ggaggctgaa gatgctgcca cttattactg ccaacagtgg 1440
 agtagtaacc cgctcacgtt cggtggcggg accaaggtgg agatcaaa 1488

<210> 259
 <211> 496
 <212> PRT
 <213> artificial sequence

<220>
 <223> 5-10VH7VL1 LHHL

<400> 259

Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
 1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
 20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
100 105 110

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
130 135 140

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
145 150 155 160

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
165 170 175

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
180 185 190

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
195 200 205

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
210 215 220

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Val Gln
245 250 255

Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys
260 265 270

Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His
275 280 285

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile
290 295 300

Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg

305 310 315 320
 Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu
 325 330 335
 Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr
 340 345 350
 Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val
 355 360 365
 Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly
 370 375 380
 Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
 385 390 395 400
 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
 405 410 415
 Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
 420 425 430
 Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro
 435 440 445
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
 450 455 460
 Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 465 470 475 480
 Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 485 490 495

<210> 260
 <211> 1491
 <212> DNA
 <213> artificial sequence

<220>
 <223> 5-10VH7VL1 HLHL

<400> 260
 gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggcctgggac ttcagtgaag 60
 atatcctgca aggcttctgg atacgccttc actaactact ggctagggttg ggtaaagcag 120


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aggcctggac atggacttga gtggattgga gatattttcc ctggaagtgg taatatccac 180
tacaatgaga agttcaaggg caaagccaca ctgactgcag acaaattctc gagcacagcc 240
tatatgcagc tcagtagcct gacatttgag gactctgctg tctatttctg tgcaagactg 300
aggaactggg acgagcctat ggactactgg ggccaaggga ccacggtcac cgtctcctca 360
ggtggtggtg gttctggcgg cggcggtcc ggtggtggtg gttctgagct cgtgatgaca 420
cagtctccat cctccctgac tgtgacagca ggagagaagg tcactatgag ctgcaagtcc 480
agtcagagtc tgttaaacag tggaaatcaa aagaactact tgacctggtg ccagcagaaa 540
ccagggcagc ctctaaact gttgatctac tgggcatcca ctagggaatc tggggtcctt 600
gatcgcttca caggcagtgg atctggaaca gatttcactc tcaccatcag cagtgtgcag 660
gctgaagacc tggcagttta ttactgtcag aatgattata gttatccgct cacgttcggt 720
gctgggacca agcttgagat caaatccgga ggtggtggat ccgacgtcca actggtgcag 780
tcaggggctg aagtgaaaaa acctggggcc tcagtgaagg tgtcctgcaa ggcttctggc 840
tacaccttta ctaggtacac gatgcaactg gtaaggcagg cacctggaca gggctctggaa 900
tggattggat acattaatcc tagccgtggt tatactaatt acaatcagaa gttcaaggac 960
cgcgtcacaa tcactacaga caaatccacc agcacagcct acatggaact gagcagcctg 1020
cgttctgagg aactgcagt ctattactgt gcaagatatt atgatgatca ttactgcctt 1080
gactactggg gccaaaggc caccggtcacc gtctcctcag gcgaaggtag tagtactggt 1140
tctggtggaa gtggagggtc aggtggagca gacgacattc agatgaccca gtctccatct 1200
agcctgtctg catctgtcgg ggaccgtgtc accatcacct gcagagccag tcaaagtgtg 1260
agttacatga actggtacca gcagaagccg ggcaaggcac caaaagatg gatttatgac 1320
acatccaaag tggttcttgg agtccctgct cgcttcagtg gcagtgggtc tgggaccgac 1380
tactctctca caatcaacag cttggaggct gaagatgctg ccacttatta ctgccaacag 1440
tggagtagta acccgctcac gttcggtggc gggaccaagg tggagatcaa a 1491

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<210> 261

<211> 497

<212> PRT

<213> artificial sequence

<220>

<223> 5-10VH7VL1 HLHL

<400> 261

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly

1	5	10	15
Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn	20	25	30
Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp	35	40	45
Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys	50	55	60
Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala	65	70	75
Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe	85	90	95
Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln	100	105	110
Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly	115	120	125
Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser	130	135	140
Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser	145	150	155
Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp	165	170	175
Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala	180	185	190
Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser	195	200	205
Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu	210	215	220
Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly	225	230	235
			240

Ala Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Val
245 250 255

Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val
260 265 270

Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met
275 280 285

His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
290 295 300

Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp
305 310 315 320

Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu
325 330 335

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
340 345 350

Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr
355 360 365

Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser
370 375 380

Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser Pro Ser
385 390 395 400

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
405 410 415

Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys
420 425 430

Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val
435 440 445

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr
450 455 460

Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
465 470 475 480

Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
 485 490 495

Lys

<210> 262
 <211> 1488
 <212> DNA
 <213> artificial sequence

<220>
 <223> 5-10VL1VH7 LHLH

<400> 262
 gagctcgtga tgacacagtc tccatcctcc ctgactgtga cagcaggaga gaaggctact 60
 atgagctgca agtccagtc gagtctgtta aacagtggaa atcaaaagaa ctacttgacc 120
 tgggtaccagc agaaaccagg gcagcctcct aaactgttga tctactgggc atccactagg 180
 gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc 240
 atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300
 ccgctcacgt tcggtgctgg gaccaagctt gagatcaaag gtggtggtgg ttctggcggc 360
 ggcggctccg gtggtggtgg ttctgaggtg cagctgctcg agcagtctgg agctgagctg 420
 gtaaggcctg ggacttcagt gaagatatcc tgcaaggctt ctggatacgc cttcactaac 480
 tactggctag gttgggtaaa gcagaggcct ggacatggac ttgagtggat tggagatatt 540
 ttccctggaa gtggtaatat ccactacaat gagaagttca agggcaaagc cacactgact 600
 gcagacaaat cttcgagcac agcctatatg cagctcagta gcctgacatt tgaggactct 660
 gctgtctatt tctgtgcaag actgaggaac tgggacgagc ctatggacta ctggggccaa 720
 gggaccacgg tcaccgtctc ctccggaggt ggtggatccg acattcagat gacccagtct 780
 ccatctagcc tgtctgcac tgtcggggac cgtgtcacca tcacctgcag agccagtcaa 840
 agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcacccaa aagatggatt 900
 tatgacacat ccaaagtggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg 960
 accgactact ctctcacaat caacagcttg gaggtgaag atgctgccac ttattactgc 1020
 caacagtgga gtagtaaccc gctcacgttc ggtggcggga ccaagggtga gatcaaaggc 1080
 gaaggacta gtactggttc tgggtggaagt ggaggttcag gtggagcaga cgacgtccaa 1140
 ctggtgcagt caggggctga agtgaaaaaa cctggggcct cagtgaagggt gtcctgcaag 1200
 gcttctggct acacctttac taggtacacg atgcactggg taaggcaggc acctggacag 1260

ggtctggaat ggattggata cattaatcct agccgtgggtt atactaatta caatcagaag 1320
 ttcaaggacc gcgtcacaaat cactacagac aaatccacca gcacagccta catggaactg 1380
 agcagcctgc gttctgagga cactgcagtc tattactgtg caagatatta tgatgatcat 1440
 tactgccttg actactgggg ccaaggcacc acggtcaccg tctcctca 1488

<210> 263
 <211> 496
 <212> PRT
 <213> artificial sequence

<220>
 <223> 5-10VL1VH7 LHLH

<400> 263

Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
 1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
 20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
 85 90 95

Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
 100 105 110

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 115 120 125

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
 130 135 140

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
 145 150 155 160

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
 165 170 175

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
 180 185 190

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
 195 200 205

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
 210 215 220

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
 225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Gln
 245 250 255

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
 260 265 270

Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr
 275 280 285

Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser
 290 295 300

Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
 305 310 315 320

Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala
 325 330 335

Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly
 340 345 350

Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly Ser Gly
 355 360 365

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val Gln Ser
 370 375 380

Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
 385 390 395 400

Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln
 405 410 415

Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg
 420 425 430

Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr
 435 440 445

Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg
 450 455 460

Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His
 465 470 475 480

Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 485 490 495

<210> 264
 <211> 1491
 <212> DNA
 <213> artificial sequence

<220>
 <223> 5-10VL1VH7 HLLH

<400> 264
 gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggctggggac ttcagtgaag 60
 atatcctgca aggccttctgg atacgccttc actaactact ggctaggttg ggtaaagcag 120
 aggcctggac atggacttga gtggattgga gatattttcc ctggaagtgg taatatccac 180
 tacaatgaga agttcaaggg caaagccaca ctgactgcag acaaattctc gagcacagcc 240
 tatatgcagc tcagtagcct gacatttgag gactctgctg tctatttctg tgcaagactg 300
 aggaactggg acgagcctat ggactactgg ggccaaggga ccacgggtcac cgtctcctca 360
 ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctgagct cgtgatgaca 420
 cagtctccat cctccctgac tgtgacagca ggagagaagg tcaactatgag ctgcaagtcc 480
 agtcagagtc tgtaaacag tggaaatcaa aagaactact tgacctggta ccagcagaaa 540
 ccagggcagc ctccctaaact gttgatctac tgggcatcca ctagggaatc tggggtcctc 600
 gatcgcttca caggcagtgg atctggaaca gatttcactc tcaccatcag cagtgtgcag 660
 gctgaagacc tggcagttta ttactgtcag aatgattata gttatccgct cacgttcggt 720

gctgggacca agcttgagat caaatccgga ggtggtggat ccgacattca gatgacccag 780
 tctccatcta gcctgtctgc atctgtcggg gaccgtgtca ccatcacctg cagagccagt 840
 caaagtgtaa gttacatgaa ctggtaccag cagaagccgg gcaaggcacc caaaagatgg 900
 atttatgaca catccaaagt ggcttctgga gtccctgctc gcttcagtgg cagtgggtct 960
 gggaccgact actctctcac aatcaacagc ttggaggctg aagatgctgc cacttattac 1020
 tgccaacagt ggagtagtaa cccgctcacg ttcggtggcg ggaccaaggt ggagatcaaa 1080
 ggcgaaggta ctagtactgg ttctggtgga agtggaggtt caggtggagc agacgacgtc 1140
 caactggtgc agtcaggggc tgaagtgaaa aaacctgggg cctcagtgaa ggtgtcctgc 1200
 aaggcttctg gctacacctt tactaggtac acgatgcact gggttaaggca ggcacctgga 1260
 cagggctctgg aatggattgg atacattaat cctagccgtg gttatactaa ttacaatcag 1320
 aagttcaagg accgcgtcac aatcactaca gacaaatcca ccagcacagc ctacatggaa 1380
 ctgagcagcc tgcgttctga ggacactgca gtctattact gtgcaagata ttatgatgat 1440
 cattactgcc ttgactactg gggccaaggc accacggtca ccgtctctc a 1491

<210> 265

<211> 497

<212> PRT

<213> artificial sequence

<220>

<223> 5-10VL1VH7 HLLH

<400> 265

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
 1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
 20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
 35 40 45

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
 50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
 65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
 85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
 130 135 140

Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser
 145 150 155 160

Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp
 165 170 175

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala
 180 185 190

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
 195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
 210 215 220

Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly
 225 230 235 240

Ala Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Ile
 245 250 255

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 260 265 270

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp
 275 280 285

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr
 290 295 300

Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
 305 310 315 320

Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala

325

330

335

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly
 340 345 350

Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly Ser
 355 360 365

Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val Gln
 370 375 380

Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys
 385 390 395 400

Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg
 405 410 415

Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser
 420 425 430

Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile
 435 440 445

Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu
 450 455 460

Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp
 465 470 475 480

His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 485 490 495

Ser

<210> 266
 <211> 1488
 <212> DNA
 <213> artificial sequence

<220>
 <223> 5-10/VH7VL2 LHHL

<400> 266
 gagctcgtga tgacacagtc tccatcctcc ctgactgtga cagcaggaga gaaggtcact 60
 atgagctgca agtccagtc gagtctgtta aacagtggaa atcaaaagaa ctacttgacc 120

tggtaccagc agaaaccagg gcagcctcct aaactgttga tctactgggc atccactagg 180
gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc 240
atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300
ccgctcacgt tcggtgctgg gaccaagctt gagatcaaag gtgggtgggtg ttctggcggc 360
ggcggctcgg gtgggtgggtg ttctgagggtg cagctgctcg agcagtctgg agctgagctg 420
gtaaggcctg ggacttcagt gaagatatcc tgcaaggctt ctggatacgc cttcactaac 480
tactggctag gttgggtaaa gcagaggcct ggacatggac ttgagtggat tggagatatt 540
ttccctggaa gtggtaatat ccactacaat gagaagttca agggcaaagc cacactgact 600
gcagacaaat cttcgagcac agcctatatg cagctcagta gcctgacatt tgaggactct 660
gctgtctatt tctgtgcaag actgaggaac tgggacgagc ctatggacta ctggggccaa 720
gggaccacgg tcaccgtctc ctccggaggt ggtggatccg acgtccaact ggtgcagtca 780
ggggctgaag tgaaaaaacc tggggcctca gtgaagggtg cctgcaaggc ttctggctac 840
acctttacta ggtacacgat gcactgggta aggcaggcac ctggacaggg tctggaatgg 900
attggataca ttaatcctag ccgtgggttat actaattaca atcagaagtt caaggaccgc 960
gtcacaatca ctacagacaa atccaccagc acagcctaca tggaactgag cagcctgcgt 1020
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tactggggcc aaggcaccac ggtcaccgtc tcctcaggcg aaggtagtag tactggttct 1140
ggtggaagtg gaggttcagg tggagcagac gacattgtac tgaccagtc tccagcaact 1200
ctgtctctgt ctccagggga gcgtgccacc ctgagctgca gagccagtca aagtgttaagt 1260
tacatgaact ggtaccagca gaagccgggc aaggcaccca aaagatggat ttatgacaca 1320
tccaaagtgg cttctggagt ccctgctcgc ttcagtggca gtgggtctgg gaccgactac 1380
tctctcacia tcaacagctt ggaggtgaa gatgctgcca cttattactg ccaacagtgg 1440
agtagtaacc cgctcacgtt cggtggcggg accaaggtgg agatcaaa 1488

<210> 267

<211> 496

<212> PRT

<213> artificial sequence

<220>

<223> 5-10/VH7VL2 LHHL

<400> 267

Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly

1	5	10	15
Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser	20	25	30
Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln	35	40	45
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val	50	55	60
Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr	65	70	75
Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn	85	90	95
Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile	100	105	110
Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser	115	120	125
Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly	130	135	140
Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn	145	150	155
Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp	165	170	175
Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys	180	185	190
Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala	195	200	205
Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe	210	215	220
Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln	225	230	235
			240

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Val Gln
 245 250 255

Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys
 260 265 270

Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His
 275 280 285

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile
 290 295 300

Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg
 305 310 315 320

Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu
 325 330 335

Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr
 340 345 350

Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val
 355 360 365

Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly
 370 375 380

Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro Ala Thr
 385 390 395 400

Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser
 405 410 415

Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
 420 425 430

Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro
 435 440 445

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
 450 455 460

Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 465 470 475 480

Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 485 490 495

<210> 268
 <211> 1491
 <212> DNA
 <213> artificial sequence

<220>
 <223> 5-10/VH7VL2 HLHL

<400> 268
 gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggcctgggac ttcagtgaag 60
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 aggctgggac atggacttga gtggattgga gataatttcc ctggaagtgg taatatccac 180
 tacaatgaga agttcaaggg caaagccaca ctgactgcag acaaactcttc gagcacagcc 240
 tatatgcagc tcagtagcct gacatttgag gactctgctg tctatttctg tgcaagactg 300
 aggaactggg acgagcctat ggactactgg ggccaaggga ccacggtcac cgtctcctca 360
 ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctgagct cgtgatgaca 420
 cagtctccat cctccctgac tgtgacagca ggagagaagg tcactatgag ctgcaagtcc 480
 agtcagagtc tgtaaacag tggaaatcaa aagaactact tgacctggta ccagcagaaa 540
 ccagggcagc ctctaaact gttgatctac tgggcatcca ctagggaatc tggggtcctc 600
 gatcgcttca caggcagtgg atctggaaca gatttctctc tcaccatcag cagtgtgcag 660
 gctgaagacc tggcagttta ttactgtcag aatgattata gttatccgct cacgttcggt 720
 gctgggacca agcttgagat caaatccgga ggtggtggat ccgacgtcca actggtgcag 780
 tcaggggctg aagtgaaaaa acctggggcc tcagtgaagg tgtcctgcaa ggcttctggc 840
 tacaccttta ctaggtacac gatgcactgg gtaaggcagg cacctggaca gggctctggaa 900
 tggattggat acattaatcc tagccgtggt tatactaatt acaatcagaa gttcaaggac 960
 cgcgtcacia tcactacaga caaatccacc agcacagcct acatggaact gagcagcctg 1020
 cgttctgagg aactgcagt ctattactgt gcaagatatt atgatgatca ttactgcctt 1080
 gactactggg gccaaaggcac cacggtcacc gtctcctcag gcgaaggtag tagtactggt 1140
 tctggtggaa gtggaggttc aggtggagca gacgacattg tactgaccca gtctccagca 1200
 actctgtctc tgtctccagg ggagcgtgcc accctgagct gcagagccag tcaaagtgtg 1260
 agttacatga actggtacca gcagaagccg ggcaaggcac caaaagatg gatttatgac 1320
 acatccaaag tggcttctgg agtccctgct cgcttcagtg gcagtgggtc tgggaccgac 1380

tactctctca caatcaacag cttggaggct gaagatgctg ccacttatta ctgccaacag 1440

tggagtagta acccgctcac gttcgggtggc gggaccaagg tggagatcaa a 1491

<210> 269

<211> 497

<212> PRT

<213> artificial sequence

<220>

<223> 5-10/VH7VL2 HLHL

<400> 269

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35 40 45

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
130 135 140

Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser
145 150 155 160

Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp
165 170 175

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala
180 185 190

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
210 215 220

Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly
225 230 235 240

Ala Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Val
245 250 255

Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val
260 265 270

Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met
275 280 285

His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
290 295 300

Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp
305 310 315 320

Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu
325 330 335

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
340 345 350

Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr
355 360 365

Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser
370 375 380

Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro Ala
385 390 395 400

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
405 410 415

Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys
 420 425 430

Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val
 435 440 445

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr
 450 455 460

Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
 465 470 475 480

Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
 485 490 495

Lys

<210> 270
 <211> 1488
 <212> DNA
 <213> artificial sequence

<220>
 <223> 5-10/VL2VH7 LHLH

<400> 270
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 atgagctgca agtccagtca gagtctgtta aacagtggaa atcaaaagaa ctacttgacc 120
 tgggtaccagc agaaaccagg gcagcctcct aaactgttga tctactgggc atccactagg 180
 gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc 240
 atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300
 ccgctcacgt tcggtgctgg gaccaagctt gagatcaaag gtggtggtgg ttctggcggc 360
 ggcggtccg gtggtggtgg ttctgaggtg cagctgctcg agcagtctgg agctgagctg 420
 gtaaggcctg ggacttcagt gaagatatcc tgcaaggctt ctggatacgc cttcactaac 480
 tactggctag gttgggtaaa gcagaggcct ggacatggac ttgagtggat tggagatatt 540
 ttccctggaa gtggtaatat ccactacaat gagaagttca agggcaaagc cacactgact 600
 gcagacaaat cttcgagcac agcctatatg cagctcagta gcctgacatt tgaggactct 660
 gctgtctatt tctgtgcaag actgaggaac tgggacgagc ctatggacta ctggggccaa 720

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gggaccacgg tcaccgtctc ctccggaggt ggtggatccg acattgtact gaccagctct   780
ccagcaactc tgtctctgtc tccaggggag cgtgccaccc tgagctgcag agccagtcaa   840
agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcacccaa aagatggatt   900
tatgacacat ccaaagtggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg   960
accgactact ctctcacaat caacagcttg gaggtgaag atgctgccac ttattactgc  1020
caacagtgga gtagtaaccc gctcacgttc ggtggcgagg ccaaggtgga gatcaaaggc  1080
gaaggtacta gtactggttc tgggtggaagt ggaggttcag gtggagcaga cgacgtccaa  1140
ctggtgcagt caggggctga agtgaaaaaa cctggggcct cagtgaaggt gtccctgcaag  1200
gcttctggct acacctttac taggtacacg atgcactggg taaggcaggc acctggacag  1260
ggtctggaat ggattggata cattaatcct agccgtggtt atactaatta caatcagaag  1320
ttcaaggacc gcgtcacaat cactacagac aaatccacca gcacagccta catggaactg  1380
agcagcctgc gttctgagga cactgcagtc tattactgtg caagatatta tgatgatcat  1440
tactgccttg actactgggg ccaaggcacc acggtcacgc tctcctca   1488

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<210> 271
<211> 496
<212> PRT
<213> artificial sequence

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<220>
<223> 5-10/VL2VH7 LHLH

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<400> 271

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Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
1           5           10           15

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```

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20           25           30

```

```

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35           40           45

```

```

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50           55           60

```

```

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65           70           75           80

```

```

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
85           90           95

```

Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
 100 105 110

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 115 120 125

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
 130 135 140

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
 145 150 155 160

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
 165 170 175

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
 180 185 190

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
 195 200 205

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
 210 215 220

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
 225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Val
 245 250 255

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
 260 265 270

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr
 275 280 285

Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser
 290 295 300

Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
 305 310 315 320

Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala

325 330 335
 Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly
 340 345 350
 Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly Ser Gly
 355 360 365
 Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val Gln Ser
 370 375 380
 Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
 385 390 395 400
 Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln
 405 410 415
 Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg
 420 425 430
 Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr
 435 440 445
 Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg
 450 455 460
 Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His
 465 470 475 480
 Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 485 490 495

<210> 272

<211> 1491

<212> DNA

<213> artificial sequence

<220>

<223> 5-10/VL2VH7 HLLH

<400> 272

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 atatcctgca aggcttctgg atacgccttc actaactact ggctaggttg ggtaaagcag 120
 aggcctggac atggacttga gtggattgga gatattttcc ctggaagtgg taatatccac 180
 tacaatgaga agttcaaggg caaagccaca ctgactgcag acaaattcttc gagcacagcc 240

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tatatgcagc tcagtagcct gacatttgag gactctgctg tctatttctg tgcaagactg 300
aggaactggg acgagcctat ggactactgg ggccaaggga ccacggtcac cgtctcctca 360
ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctgagct cgtgatgaca 420
cagtctccat cctccctgac tgtgacagca ggagagaagg tcactatgag ctgcaagtcc 480
agtcagagtc tgtaaacag tggaaatcaa aagaactact tgacctggta ccagcagaaa 540
ccagggcagc ctctaaact gttgatctac tgggcatcca ctagggaatc tggggtcctc 600
gatcgcttca caggcagtgg atctggaaca gatttctctc tcaccatcag cagtgtgcag 660
gctgaagacc tggcagttta ttactgtcag aatgattata gttatccgct cacgttcggt 720
gctgggacca agcttgagat caaatccgga ggtggtggat ccgacattgt actgaccag 780
tctccagcaa ctctgtctct gtctccaggg gagcgtgcca ccctgagctg cagagccagt 840
caaagtgtaa gttacatgaa ctggtaccag cagaagccgg gcaaggcacc caaaagatgg 900
atztatgaca catccaaagt ggcttctgga gtccctgctc gcttcagtgg cagtgggtct 960
gggaccgact actctctcac aatcaacagc ttggaggctg aagatgctgc cacttattac 1020
tgccaacagt ggagtagtaa cccgctcacg ttcggtggcg ggaccaaggt ggagatcaaa 1080
ggcgaaggta ctagtactgg ttctggtgga agtggaggtt caggtggagc agacgacgtc 1140
caactggtgc agtcaggggc tgaagtgaaa aaacctgggg cctcagtgaa ggtgtcctgc 1200
aaggcttctg gctacacctt tactaggtac acgatgcact gggtaaggca ggcacctgga 1260
cagggctctg aatggattgg atacattaat cctagccgtg gttatactaa ttacaatcag 1320
aagttcaagg accgcgtcac aatcactaca gacaaatcca ccagcacagc ctacatggaa 1380
ctgagcagcc tgcgttctga ggacactgca gtctattact gtgcaagata ttatgatgat 1440
cattactgcc ttgactactg gggccaaggc accacggtca ccgtctctc a 1491

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<210> 273

<211> 497

<212> PRT

<213> artificial sequence

<220>

<223> 5-10/VL2VH7 HLLH

<400> 273

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn

20	25	30
Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp		
35	40	45
Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys		
50	55	60
Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala		
65	70	75
Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe		
85	90	95
Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln		
100	105	110
Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly		
115	120	125
Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser		
130	135	140
Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser		
145	150	155
Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp		
165	170	175
Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala		
180	185	190
Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser		
195	200	205
Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu		
210	215	220
Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly		
225	230	235
Ala Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Ile		
245	250	255

Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg
 260 265 270

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp
 275 280 285

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr
 290 295 300

Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
 305 310 315 320

Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala
 325 330 335

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly
 340 345 350

Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly Ser
 355 360 365

Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val Gln
 370 375 380

Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys
 385 390 395 400

Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg
 405 410 415

Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser
 420 425 430

Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile
 435 440 445

Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu
 450 455 460

Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp
 465 470 475 480

His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 485 490 495

Ser

<210> 274
<211> 1488
<212> DNA
<213> artificial sequence

<220>
<223> 5-10/VH7VL3 LHHL

<400> 274
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atgagctgca agtccagtc gagtctgtta aacagtggaa atcaaaagaa ctacttgacc 120
tggtaccagc agaaaccagg gcagcctcct aaactgttga tctactgggc atccactagg 180
gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc 240
atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300
ccgctcacgt tcggtgctgg gaccaagctt gagatcaaag gtggtggtgg ttctggcggc 360
ggcggctccg gtggtggtgg ttctgaggtg cagctgctcg agcagtctgg agctgagctg 420
gtaaggcctg ggacttcagt gaagatatcc tgcaaggctt ctggatacgc cttcactaac 480
tactggctag gttgggtaaa gcagaggcct ggacatggac ttgagtggat tggagatatt 540
ttccctggaa gtggtaatat ccactacaat gagaagttca agggcaaagc cacactgact 600
gcagacaaat cttcgagcac agcctatatg cagctcagta gcctgacatt tgaggactct 660
gctgtctatt tctgtgcaag actgaggaac tgggacgagc ctatggacta ctggggccaa 720
gggaccacgg tcaccgtctc ctccggaggt ggtggatccg acgtccaact ggtgcagtca 780
ggggctgaag tgaaaaaacc tggggcctca gtgaagggtg cctgcaaggc ttctggctac 840
acctttacta ggtacacgat gcactgggta aggcaggcac ctggacaggg tctggaatgg 900
attggataca ttaatcctag ccgtgggttat actaattaca atcagaagtt caaggaccgc 960
gtcacaatca ctacagacaa atccaccagc acagcctaca tggaactgag cagcctgcgt 1020
tctgaggaca ctgcagtcta ttactgtgca agatattatg atgataccta ctgccttgac 1080
tactggggcc aaggcaccac ggtcaccgtc tcctcaggcg aaggtagtag tactggttct 1140
ggtggaagtg gaggttcagg tggagcagac gacattgtac tgaccagtc tccagcaact 1200
ctgtctctgt ctccagggga gcgtgccacc ctgacctgca gagccagttc aagtgttaagt 1260
tacatgaact ggtaccagca gaagccgggc aaggcaccca aaagatggat ttatgacaca 1320
tccaaagtgg cttctggagt ccctgctcgc ttcagtggca gtgggtctgg gaccgactac 1380

tctctcaciaa tcaacagctt ggaggctgaa gatgctgcca cttattactg ccaacagtgg 1440

agtagtaacc cgctcacgtt cgggtggcggg accaaggtgg agatcaaa 1488

<210> 275

<211> 496

<212> PRT

<213> artificial sequence

<220>

<223> 5-10/VH7VL3 LHHL

<400> 275

Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
100 105 110

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
130 135 140

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
145 150 155 160

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
165 170 175

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
 180 185 190

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
 195 200 205

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
 210 215 220

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
 225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Val Gln
 245 250 255

Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys
 260 265 270

Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His
 275 280 285

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile
 290 295 300

Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg
 305 310 315 320

Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu
 325 330 335

Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr
 340 345 350

Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val
 355 360 365

Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser Gly
 370 375 380

Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro Ala Thr
 385 390 395 400

Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser
 405 410 415

Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
 420 425 430

Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro
 435 440 445

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
 450 455 460

Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 465 470 475 480

Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 485 490 495

<210> 276

<211> 1491

<212> DNA

<213> artificial sequence

<220>

<223> 5-10/VH7VL3 HLHL

<400> 276

gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggcctgggac ttcagtgaag	60
atatactgca aggccttctgg atacgccttc actaactact ggctaggttg ggtaaagcag	120
aggcctggac atggacttga gtggattgga gatattttcc ctggaagtgg taatatccac	180
tacaatgaga agttcaaggg caaagccaca ctgactgcag acaaattcttc gagcacagcc	240
tatatgcagc tcagtagcct gacatttgag gactctgctg tctatttctg tgcaagactg	300
aggaactggg acgagcctat ggactactgg ggccaaggga ccacggtcac cgtctcctca	360
ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctgagct cgtgatgaca	420
cagtctccat cctccctgac tgtgacagca ggagagaagg tcactatgag ctgcaagtcc	480
agtcagagtc tgtaaagcag tggaaatcaa aagaactact tgacctggta ccagcagaaa	540
ccagggcagc ctctaaact gttgatctac tgggcatcca ctagggaatc tggggtccct	600
gatcgcttca caggcagtgg atctggaaca gatttcactc tcaccatcag cagtgtgcag	660
gctgaagacc tggcagttta ttactgtcag aatgattata gttatccgct cacgttcggt	720
gctgggacca agcttgagat caaatccgga ggtggtggat ccgacgtcca actggtgcag	780
tcaggggctg aagtgaaaaa acctggggcc tcagtgaagg tgtcctgcaa ggcttctggc	840

```

tacaacttta ctaggtacac gatgcactgg gtaaggcagg cacctggaca gggctctggaa    900
tggattggat acattaatcc tagccgtggt tatactaatt acaatcagaa gttcaaggac    960
cgcgtcacaa tcactacaga caaatccacc agcacagcct acatggaact gagcagcctg   1020
cggtctgagg aactgcagt ctattactgt gcaagatatt atgatgatca ttactgcctt   1080
gactactggg gccaaaggcac cacgggtcac gtctcctcag gcgaaggtac tagtactggt   1140
tctgggtggaa gtggaggttc aggtggagca gacgacattg tactgaccca gtctccagca   1200
actctgtctc tgtctccagg ggagcgtgcc accctgacct gcagagccag ttcaagtgta   1260
agttacatga actggtacca gcagaagccg ggcaaggcac caaaagatg gatttatgac   1320
acatccaaag tggcttctgg agtccctgct cgcttcagtg gcagtgggtc tgggaccgac   1380
tactctctca caatcaacag cttggaggct gaagatgctg ccacttatta ctgccaacag   1440
tggagtagta acccgctcac gttcgggtggc gggaccaagg tggagatcaa a         1491

```

```

<210> 277
<211> 497
<212> PRT
<213> artificial sequence

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<220>
<223> 5-10/VH7VL3 HLHL

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<400> 277

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```

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1           5           10           15

```

```

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
           20           25           30

```

```

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35           40           45

```

```

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
50           55           60

```

```

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65           70           75           80

```

```

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
85           90           95

```

```

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
100           105           110

```

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
 130 135 140

Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser
 145 150 155 160

Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp
 165 170 175

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala
 180 185 190

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
 195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
 210 215 220

Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly
 225 230 235 240

Ala Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Val
 245 250 255

Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val
 260 265 270

Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met
 275 280 285

His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
 290 295 300

Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp
 305 310 315 320

Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu
 325 330 335

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg

340

345

350

Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr
 355 360 365

Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly Gly Ser
 370 375 380

Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser Pro Ala
 385 390 395 400

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys Arg Ala
 405 410 415

Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys
 420 425 430

Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val
 435 440 445

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr
 450 455 460

Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
 465 470 475 480

Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
 485 490 495

Lys

<210> 278

<211> 1488

<212> DNA

<213> artificial sequence

<220>

<223> 5-10/VL3VH7 LHLH

<400> 278

gagctcgtga tgacacagtc tccatcctcc ctgactgtga cagcaggaga gaaggtcact 60

atgagctgca agtccagtc gagtctgtta aacagtggaa atcaaaagaa ctacttgacc 120

tggtaccagc agaaaccagg gcagcctcct aaactgttga tctactgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300
 ccgctcacgt tcggtgctgg gaccaagctt gagatcaaag gtggtggtgg ttctggcggc 360
 ggcggctccg gtggtggtgg ttctgaggtg cagctgctcg agcagtctgg agctgagctg 420
 gtaaggcctg ggacttcagt gaagatatcc tgcaaggctt ctggatacgc cttcactaac 480
 tactggctag gttgggtaaa gcagaggcct ggacatggac ttgagtggat tggagatatt 540
 ttccctggaa gtggtaatat ccactacaat gagaagttca agggcaaagc cacactgact 600
 gcagacaaat cttcgagcac agcctatatg cagctcagta gcctgacatt tgaggactct 660
 gctgtctatt tctgtgcaag actgaggaac tgggacgagc ctatggacta ctggggccaa 720
 gggaccacgg tcaccgtctc ctccggaggt ggtggatccg acattgtact gacccagtct 780
 ccagcaactc tgtctctgtc tccaggggag cgtgccaccc tgacctgcag agccagttca 840
 agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcacccaa aagatggatt 900
 tatgacacat ccaaagtggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg 960
 accgactact ctctcacaat caacagcttg gaggtgaag atgctgccac ttattactgc 1020
 caacagtgga gtagtaaccc gctcacgttc ggtggcgagg ccaaggtgga gatcaaaggc 1080
 gaaggtacta gtactggttc tgggtggaagt ggaggttcag gtggagcaga cgacgtccaa 1140
 ctggtgcagt caggggctga agtgaaaaaa cctggggcct cagtgaaggt gtccctgcaag 1200
 gcttctggct acacctttac taggtacacg atgcactggg taaggcaggc acctggacag 1260
 ggtctggaat ggattggata cattaatcct agccgtgggt atactaatta caatcagaag 1320
 ttcaaggacc gcgtcacaat cactacagac aaatccacca gcacagccta catggaactg 1380
 agcagcctgc gttctgagga cactgcagtc tattactgtg caagatatta tgatgatcat 1440
 tactgccttg actactgggg ccaaggcacc acggtcaccg tctcctca 1488

<210> 279

<211> 496

<212> PRT

<213> artificial sequence

<220>

<223> 5-10/VL3VH7 LHLH

<400> 279

Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
 1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser

20					25					30					
Gly	Asn	Gln	Lys	Asn	Tyr	Leu	Thr	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln
	35						40					45			
Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu	Ser	Gly	Val
	50					55					60				
Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr
	65					70					75				80
Ile	Ser	Ser	Val	Gln	Ala	Glu	Asp	Leu	Ala	Val	Tyr	Tyr	Cys	Gln	Asn
				85					90					95	
Asp	Tyr	Ser	Tyr	Pro	Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Ile
			100					105					110		
Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
		115					120					125			
Glu	Val	Gln	Leu	Leu	Glu	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly
	130					135					140				
Thr	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ala	Phe	Thr	Asn
	145					150					155				160
Tyr	Trp	Leu	Gly	Trp	Val	Lys	Gln	Arg	Pro	Gly	His	Gly	Leu	Glu	Trp
				165					170					175	
Ile	Gly	Asp	Ile	Phe	Pro	Gly	Ser	Gly	Asn	Ile	His	Tyr	Asn	Glu	Lys
			180					185					190		
Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser	Thr	Ala
		195					200					205			
Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Phe	Glu	Asp	Ser	Ala	Val	Tyr	Phe
	210					215					220				
Cys	Ala	Arg	Leu	Arg	Asn	Trp	Asp	Glu	Pro	Met	Asp	Tyr	Trp	Gly	Gln
	225					230					235				240
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Val
				245					250					255	

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
 260 265 270

Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr
 275 280 285

Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser
 290 295 300

Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
 305 310 315 320

Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala
 325 330 335

Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly
 340 345 350

Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly Ser Gly
 355 360 365

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val Gln Ser
 370 375 380

Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
 385 390 395 400

Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln
 405 410 415

Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg
 420 425 430

Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr
 435 440 445

Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg
 450 455 460

Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His
 465 470 475 480

Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 485 490 495

<210> 280
 <211> 1491
 <212> DNA
 <213> artificial sequence

<220>
 <223> 5-10/VL3VH7 HLLH

<400> 280
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 atatcctgca aggttcttgg atacgccttc actaactact ggctaggttg ggtaaagcag 120
 aggcctggac atggacttga gtggattgga gatattttcc ctggaagtgg taatatccac 180
 tacaatgaga agttcaaggg caaagccaca ctgactgcag acaaattcttc gagcacagcc 240
 tatatgcagc tcagtagcct gacatttgag gactctgctg tctatttctg tgcaagactg 300
 aggaactggg acgagcctat ggactactgg ggccaaggga ccacggtcac cgtctcctca 360
 ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctgagct cgtgatgaca 420
 cagtctccat cctccctgac tgtgacagca ggagagaagg tcactatgag ctgcaagtcc 480
 agtcagagtc tgttaaacag tggaaatcaa aagaactact tgacctggta ccagcagaaa 540
 ccagggcagc ctcttaaact gttgatctac tgggcatcca ctagggaatc tggggtcctc 600
 gatcgcttca caggcagtgg atctggaaca gatttactc tcaccatcag cagtgtgcag 660
 gctgaagacc tggcagttta ttactgtcag aatgattata gttatccgct cacgttcggt 720
 gctgggacca agcttgagat caaatccgga ggtggtggat ccgacattgt actgaccag 780
 tctccagcaa ctctgtctct gtctccaggg gagcgtgcca ccctgacctg cagagccagt 840
 tcaagtgtaa gttacatgaa ctggtaccag cagaagccgg gcaaggcacc caaaagatgg 900
 atttatgaca catccaaagt ggcttctgga gtcctgctc gcttcagtgg cagtgggtct 960
 gggaccgact actctctcac aatcaacagc ttggaggctg aagatgctgc cacttattac 1020
 tgccaacagt ggagtagtaa cccgctcagc ttcgggtggc ggaccaaggt ggagatcaaa 1080
 ggcgaaggta ctagtactgg ttctggtgga agtggaggtt caggtggagc agacgacgtc 1140
 caactggtgc agtcaggggc tgaagtgaaa aaacctgggg cctcagtga ggtgtcctgc 1200
 aaggcttctg gctacacctt tactaggtac acgatgcact gggtaaggca ggcacctgga 1260
 cagggtctgg aatggattgg atacattaat cctagccgtg gttataactaa ttacaatcag 1320
 aagttcaagg accgcgtcac aatcactaca gacaaatcca ccagcacagc ctacatggaa 1380
 ctgagcagcc tgcgttctga ggacactgca gtctattact gtgcaagata ttatgatgat 1440
 cattactgcc ttgactactg gggccaaggc accacggtca ccgtctcctc a 1491

<210> 281
 <211> 497
 <212> PRT
 <213> artificial sequence

<220>
 <223> 5-10/VL3VH7 HLLH

<400> 281

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
 1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
 20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
 35 40 45

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
 50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
 65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
 85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
 130 135 140

Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser
 145 150 155 160

Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp
 165 170 175

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala
 180 185 190

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
 195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
 210 215 220

Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly
 225 230 235 240

Ala Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Ile
 245 250 255

Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg
 260 265 270

Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
 275 280 285

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr
 290 295 300

Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
 305 310 315 320

Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala
 325 330 335

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly
 340 345 350

Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly Ser
 355 360 365

Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val Gln
 370 375 380

Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys
 385 390 395 400

Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg
 405 410 415

Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser
 420 425 430

Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile
 435 440 445

Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu
 450 455 460

Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp
 465 470 475 480

His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 485 490 495

Ser

<210> 282
 <211> 1497
 <212> DNA
 <213> artificial sequence

<220>
 <223> VL1/VH5x4-7 LHHL

<400> 282
 gacattcaga tgaccagtc tccatctagc ctgtctgcat ctgtcgggga ccgtgtcacc 60
 atcacctgca gagccagtca aagtgttaagt tacatgaact ggtaccagca gaagccgggc 120
 aaggcaccga aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
 ttcagtggca gtgggtctgg gaccgactac tctctcaca tcaacagctt ggaggctgaa 240
 gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cgggtggcggg 300
 accaaggtgg agatcaaagg cgaaggtact agtactggtt ctggtggaag tggaggttca 360
 ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
 tcagtgaagg tgtctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
 gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggt 540
 tatactaatt acgcagacag cgtcaagggc cgcttcacaa tcaactacaga caaatccacc 600
 agcacagcct acatggaact gagcagcctg cgcttctgagg aactgcaac ctattactgt 660
 gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc 720
 gtctcctccg gaggtgggtg atccgaggtg cagctgctcg agcagtctgg agctgagctg 780
 gcgaggcctg gggcttcagt gaagctgtcc tgcaaggctt ctggctacac cttcacaac 840

tatgggtttaa gctgggtgaa gcagaggcct ggacagggtcc ttgagtggat tggagaggtt 900
 tatcctagaa ttggtaatgc ttactacaat gagaagttca agggcaaggc cacactgact 960
 gcagacaaat cctccagcac agcgtccatg gagctccgca gcctgacctc tgaggactct 1020
 gcggtctatt tctgtgcaag acgggggatcc tacgatacta actacgactg gtacttcgat 1080
 gtctggggcc aaggggaccac ggtcaccgtc tcctcagggtg gtggtggttc tggcggcggc 1140
 ggctccggtg gtggtggttc tgagctcgtg atgaccaga ctccactctc cctgcctgtc 1200
 agtcttggag atcaagcctc catctcttgc agatctagtc agagccttgt acacagtaat 1260
 ggaaacacct atttacattg gtacctgcag aagccaggcc agtctccaaa gctcctgac 1320
 taaaagttt ccaaccgatt ttctggggtc ccagacaggt tcagtggcag tggatcaggg 1380
 acagatttca cactcaagat cagcagagtg gaggctgagg atctgggagt ttatttctgc 1440
 tctcaaagta cacatgttcc gtacacgttc ggagggggga ccaagcttga gatcaaa 1497

<210> 283

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> VL1/VH5x4-7 LHHL

<400> 283

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
 20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
 35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
 100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
 115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
 145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe
 180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr
 210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser
 245 250 255

Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys
 260 265 270

Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln
 275 280 285

Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile
 290 295 300

Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr
 305 310 315 320

Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr
 325 330 335

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp

340

345

350

Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val
 385 390 395 400

Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
 405 410 415

Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
 420 425 430

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
 435 440 445

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 450 455 460

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
 465 470 475 480

Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
 485 490 495

Glu Ile Lys

<210> 284

<211> 1500

<212> DNA

<213> artificial sequence

<220>

<223> VH5/VL1x4-7 HLHL

<400> 284

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tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120

cctggacagg gtctggaatg gattggatac attaactcta gccgtgggta tactaattac 180

gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240


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atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctccctcagge 360
gaagg tacta gtactggttc tgggtggaagt ggagggttcag gtggagcaga cgacattcag 420
atgacccagt ctccatctag cctgtctgca tctgtcgggg accgtgtcac catcacctgc 480
agagccagtc aaagtgtgaa ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg 720
gagatcaaat ccggagggtg tggatccgag gtgcagctgc tcgagcagtc tggagctgag 780
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aactatggtt taagctgggt gaagcagagg cctggacagg tccttgagtg gattggagag 900
gtttatccta gaattggtaa tgcttactac aatgagaagt tcaagggcaa ggccacactg 960
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tctgcggtct atttctgtgc aagacgggga tcctacgata ctaactacga ctggtacttc 1080
gatgtctggg gccaaaggac cacggtcacc gtctcctcag gtggtggtgg ttctggcggc 1140
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gtcagtcttg gagatcaagc ctccatctct tgcagatcta gtcagagcct tgtacacagt 1260
aatggaaaca cctattttaca ttggtacctg cagaagccag gccagtctcc aaagctcctg 1320
atctacaaag tttccaaccg attttctggg gtcccagaca ggttcagtgg cagtggatca 1380
gggacagatt tcacactcaa gatcagcaga gtggaggctg aggatctggg agttttatttc 1440
tgctctcaaa gtacacatgt tccgtacacg ttcggagggg ggaccaagct tgagatcaaa 1500

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<210> 285

<211> 500

<212> PRT

<213> artificial sequence

<220>

<223> VH5/VL1x4-7 HLHL

<400> 285

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Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1           5           10          15

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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr

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20					25					30					
Thr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile
		35					40					45			
Gly	Tyr	Ile	Asn	Pro	Ser	Arg	Gly	Tyr	Thr	Asn	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Thr	Thr	Asp	Lys	Ser	Thr	Ser	Thr	Ala	Tyr
65				70					75					80	
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Thr	Tyr	Tyr	Cys
			85					90					95		
Ala	Arg	Tyr	Tyr	Asp	Asp	His	Tyr	Cys	Leu	Asp	Tyr	Trp	Gly	Gln	Gly
		100						105					110		
Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Glu	Gly	Thr	Ser	Thr	Gly	Ser	Gly
		115					120					125			
Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ala	Asp	Asp	Ile	Gln	Met	Thr	Gln	Ser
	130					135					140				
Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys
145				150					155					160	
Arg	Ala	Ser	Gln	Ser	Val	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Pro
			165						170					175	
Gly	Lys	Ala	Pro	Lys	Arg	Trp	Ile	Tyr	Asp	Thr	Ser	Lys	Val	Ala	Ser
		180						185					190		
Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Ser
	195						200					205			
Leu	Thr	Ile	Asn	Ser	Leu	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys
	210					215					220				
Gln	Gln	Trp	Ser	Ser	Asn	Pro	Leu	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val
225				230						235				240	
Glu	Ile	Lys	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Val	Gln	Leu	Leu	Glu	Gln
			245					250						255	

Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys
 260 265 270

Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys
 275 280 285

Gln Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg
 290 295 300

Ile Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu
 305 310 315 320

Thr Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu
 325 330 335

Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr
 340 345 350

Asp Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr
 355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380

Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu Pro
 385 390 395 400

Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
 405 410 415

Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys
 420 425 430

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
 435 440 445

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
 450 455 460

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe
 465 470 475 480

Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys
 485 490 495

Leu Glu Ile Lys
500

<210> 286
<211> 1497
<212> DNA
<213> artificial sequence

<220>
<223> VL1/VH5x4-7 LHLH

<400> 286
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atcacctgca gagccagtca aagtgttaagt tacatgaact ggtaccagca gaagccgggc 120
aaggcaccga aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cgggtggcggg 300
accaaggtgg agatcaaagg cgaaggtact agtactggtt ctggtggaag tggaggttca 360
ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
gtaaggcagg cacctggaca ggggtctggaa tggattggat acattaatcc tagccgtggt 540
tatactaatt acgcagacag cgtcaagggc cgcttcacia tcactacaga caaatccacc 600
agcacagcct acatggaact gagcagcctg cgcttctgagg aactgcaac ctattactgt 660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc 720
gtctcctccg gaggtggtgg atccgagctc gtgatgacct agactccact ctccctgcct 780
gtcagtcttg gagatcaagc ctccatctct tgcagatcta gtcagagcct tgtacacagt 840
aatggaaaca cctattttaca ttggtacctg cagaagccag gccagtctcc aaagctcctg 900
atctacaaag ttccaaccg attttctggg gtcccagaca ggttcagtgg cagtggatca 960
gggacagatt tcacactcaa gatcagcaga gtggaggctg aggatctggg agttttatttc 1020
tgctctcaaa gtacacatgt tccgtacacg ttcggagggg ggaccaagct tgagatcaaa 1080
ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctgaggt gcagctgctc 1140
gagcagtctg gagctgagct ggcgaggcct ggggcttcag tgaagctgtc ctgcaaggct 1200
tctggctaca ccttcacaaa ctatggttta agctgggtga agcagaggcc tggacaggtc 1260
cttgagtgga ttggagaggt ttatcctaga attggtaatg cttactacaa tgagaagttc 1320
aagggaagg ccacactgac tgcagacaaa tctccagca cagcgtccat ggagctccgc 1380

agcctgacct ctgaggactc tgcggtctat ttctgtgcaa gacggggatc ctacgatact 1440

aactacgact ggtacttcga tgtctggggc caagggacca cggtcacccgt ctcctca 1497

<210> 287

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> VL1/VH5x4-7 LHLH

<400> 287

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe
 180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr
 210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro
 245 250 255

Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg
 260 265 270

Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp
 275 280 285

Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val
 290 295 300

Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser
 305 310 315 320

Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu
 325 330 335

Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly
 340 345 350

Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly
 355 360 365

Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser Gly
 370 375 380

Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala
 385 390 395 400

Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln Arg
 405 410 415

Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile Gly
 420 425 430

Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala
 435 440 445

Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr Ser
 450 455 460

Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp Thr
 465 470 475 480

Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val Thr
 485 490 495

Val Ser Ser

<210> 288

<211> 1500

<212> DNA

<213> artificial sequence

<220>

<223> VH5/VL1x4-7 HLLH

<400> 288

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cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac	180
gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac	240
atggaactga gcagcctgcy ttctgaggac actgcaacct attactgtgc aagatattat	300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc	360
gaaggctacta gtactgggtc tggtggaagt ggaggttcag gtggagcaga cgacattcag	420
atgacccagt ctccatctag cctgtctgca tctgtcgggg accgtgtcac catcacctgc	480
agagccagtc aaagtgtgaa ttacatgaac tgggtaccagc agaagccggg caaggcaccc	540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc	600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc	660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaagggtg	720

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gagatcaaat ccggagggtgg tggatccgag ctctgtgatga cccagactcc actctccctg      780
cctgtcagtc ttggagatca agcctccatc tcttgcatat ctagtcagag ccttgtagac      840
agtaatggaa acacctatatt acattggtac ctgcagaagc caggccagtc tccaaagctc      900
ctgatctaca aagtttccaa ccgattttct ggggtcccag acaggttcag tggcagtggg      960
tcagggacag atttcacact caagatcagc agagtggagg ctgaggatct gggagtttat     1020
ttctgtcttc aaagtacaca tgttccgtac acgttcggag gggggaccaa gcttgagatc     1080
aaagggtggtg gtggttcttg cggcggcggc tccggtggtg gtggttctga ggtgcagctg     1140
ctcgagcagt ctggagctga gctggcgagg cctggggctt cagtgaagct gtcctgcaag     1200
gcttctggct acaccttcac aaactatggt ttaagctggg tgaagcagag gcctggacag     1260
gtccttgagt ggattggaga ggtttatcct agaattggta atgcttacta caatgagaag     1320
ttcaagggca aggccacact gactgcagac aaatcctcca gcacagcgtc catggagctc     1380
cgcagcctga cctctgagga ctctgcggtc tatttctgtg caagacgggg atcctacgat     1440
actaactacg actggtactt cgatgtctgg ggccaaggga ccacgggtcac cgtctcctca     1500

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<210> 289
<211> 500
<212> PRT
<213> artificial sequence

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<220>
<223> VH5/VL1x4-7 HLLH

```

```

<400> 289

```

```

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1           5           10           15

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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20           25           30

```

```

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35           40           45

```

```

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
50           55           60

```

```

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65           70           75           80

```

```

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85           90           95

```


Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser
 130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
 145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr
 245 250 255

Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys
 260 265 270

Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His
 275 280 285

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys
 290 295 300

Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
 305 310 315 320

Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp

325

330

335

Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe
 340 345 350

Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly
 355 360 365

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser
 370 375 380

Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys
 385 390 395 400

Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln
 405 410 415

Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile
 420 425 430

Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr
 435 440 445

Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr
 450 455 460

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp
 465 470 475 480

Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val
 485 490 495

Thr Val Ser Ser
 500

<210> 290

<211> 1497

<212> DNA

<213> artificial sequence

<220>

<223> VL2/VH5x4-7 LHHL

<400> 290

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ctgagctgca gagccagtca aagtgttaagt tacatgaact ggtaccagca gaagccgggc 120

```

aaggcaccca aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cgggtggcggg 300
accaaggtgg agatcaaagg cgaagggtact agtactgggt ctggtggaag tggaggttca 360
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tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
gtaaggcagg cacctggaca ggggtctggaa tggattggat acattaatcc tagccgtggg 540
tatactaatt acgcagacag cgtcaagggc cgcttcacia tcactacaga caaatccacc 600
agcacagcct acatggaact gagcagcctg cgcttctgagg aactgcaac ctattactgt 660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc 720
gtctcctccg gaggtgggtg atccgaggtg cagctgctcg agcagtctgg agctgagctg 780
gcgaggcctg gggcttcagt gaagctgtcc tgcaaggctt ctggctacac cttcaciaaac 840
tatggtttaa gctgggtgaa gcagaggcct ggacaggctc ttgagtggat tggagaggtt 900
tactctagaa ttggtaatgc ttactacaat gagaagttca agggcaaggc cacactgact 960
gcagacaaat cctccagcac agcgtccatg gagctccgca gcctgacctc tgaggactct 1020
gcggtctatt tctgtgcaag acggggatcc tacgatacta actacgactg gtacttcgat 1080
gtctggggcc aagggaaccac ggtcaccgtc tcctcaggtg gtggtggttc tggcggcggc 1140
ggctccggtg gtggtggttc tgagctcgtg atgaccaga ctccactctc cctgcctgtc 1200
agtcttgag atcaagcctc catctcttgc agatctagtc agagccttgt acacagtaat 1260
ggaaacacct atttacattg gtacctgcag aagccaggcc agtctccaaa gctcctgatc 1320
taciaagttt ccaaccgatt ttctggggtc ccagacaggt tcagtggcag tggatcaggg 1380
acagatttca cactcaagat cagcagagtg gaggtgagg atctgggagt ttatttctgc 1440
tctcaaagta cacatgttcc gtacacgttc ggagggggga ccaagcttga gatcaaa 1497

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<210> 291

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> VL2/VH5x4-7 LHHL

<400> 291

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly

1	5	10	15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met	20	25	30
Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr	35	40	45
Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser	50	55	60
Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu	65	70	75
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr	85	90	95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr	100	105	110
Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu	115	120	125
Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val	130	135	140
Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp	145	150	155
Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn	165	170	175
Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe	180	185	190
Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser	195	200	205
Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr	210	215	220
Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr	225	230	235
			240

Val Ser Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser
 245 250 255

Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys
 260 265 270

Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln
 275 280 285

Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile
 290 295 300

Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr
 305 310 315 320

Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr
 325 330 335

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp
 340 345 350

Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val
 385 390 395 400

Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
 405 410 415

Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
 420 425 430

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
 435 440 445

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 450 455 460

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
 465 470 475 480

Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
 485 490 495

Glu Ile Lys

<210> 292
 <211> 1497
 <212> DNA
 <213> artificial sequence

<220>
 <223> VL2/VH5x4-7 LHLH

<400> 292
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 aaggcaccga aaagatggat ttatgacaca tccaaagtgg cttctggagt cctgctcgc 180
 ttcagtggca gtgggtctgg gacogactac tctctcacia tcaacagctt ggaggctgaa 240
 gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cgggtggcggg 300
 accaagggtg agatcaaagg cgaaggtact agtactgggt ctggtggaag tggaggttca 360
 ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
 tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
 gtaaggcagg cacctggaca ggggtctggaa tggattggat acattaatcc tagccgtggg 540
 tatactaatt acgcagacag cgtcaagggc cgcttcacaa tctactacaga caaatccacc 600
 agcacagcct acatggaact gagcagcctg cgcttctgagg aactgcaac ctattactgt 660
 gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc 720
 gtctcctccg gaggtgggtg atccgagctc gtgatgacct agactccact ctccctgcct 780
 gtcagtcttg gagatcaagc ctccatctct tgcagatcta gtcagagcct tgtacacagt 840
 aatggaaaca cctattttaca ttggtacctg cagaagccag gccagtctcc aaagctcctg 900
 atctacaaag tttccaaccg attttctggg gtcccagaca ggttcagtgg cagtggatca 960
 gggacagatt tcacactcaa gatcagcaga gtggaggctg aggatctggg agttttatttc 1020
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 ggtggtggtg gttctggcgg cggcgggctcc ggtggtggtg gttctgaggt gcagctgctc 1140
 gagcagtctg gagctgagct ggcgaggcct ggggcttcag tgaagctgtc ctgcaaggct 1200
 tctggctaca ccttcacaaa ctatggttta agctgggtga agcagaggcc tggacaggtc 1260

cttgagtgga ttggagaggt ttatcctaga attggtaatg cttactacaa tgagaagttc 1320
aagggcaagg ccacactgac tgcagacaaa tcctccagca cagcgtccat ggagctccgc 1380
agcctgacct ctgaggactc tgcggtctat ttctgtgcaa gacggggatc ctacgatact 1440
aactacgact ggtacttcga tgtctggggc caagggacca cggtcaccgt ctcctca 1497

<210> 293
<211> 499
<212> PRT
<213> artificial sequence

<220>
<223> VL2/VH5x4-7 LHLH

<400> 293

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe
 180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr
 210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro
 245 250 255

Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg
 260 265 270

Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp
 275 280 285

Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val
 290 295 300

Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser
 305 310 315 320

Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu
 325 330 335

Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly
 340 345 350

Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly
 355 360 365

Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser Gly
 370 375 380

Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala
 385 390 395 400

Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln Arg
 405 410 415

Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile Gly
 420 425 430

Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala
 435 440 445

Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr Ser
 450 455 460

Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp Thr
 465 470 475 480

Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val Thr
 485 490 495

Val Ser Ser

<210> 294
 <211> 1497
 <212> DNA
 <213> artificial sequence

<220>
 <223> VL3VH5x4-7 LHHL

<400> 294
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 aaggcaccca aaagatggat ttatgacaca tccaaagtgg cttctggagt ccttgctcgc 180
 ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
 gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cgggtggcggg 300
 accaaggtgg agatcaaagg cgaaggtact agtactggtt ctggtggaag tggaggttca 360
 ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
 tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
 gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggg 540
 tatactaatt acgcagacag cgtcaagggc cgcttcacia tcaactacaga caaatccacc 600

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agcacagcct acatggaact gagcagcctg cgttctgagg aactgcaac ctattactgt    660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc    720
gtctcctccg gaggtggtgg atccgagggtg cagctgctcg agcagtctgg agctgagctg    780
gcgaggcctg gggcttcagt gaagctgtcc tgcaaggctt ctggctacac cttcacaaac    840
tatggtttaa gctgggtgaa gcagaggcct ggacaggctc ttgagtggat tggagagggt    900
tattctagaa ttggaatgc ttactacaat gagaagttca agggcaaggc cacactgact    960
gcagacaaat cctccagcac agcgtccatg gagctccgca gcctgacctc tgaggactct   1020
gcggtctatt tctgtgcaag acggggatcc tacgatacta actacgactg gtacttcgat   1080
gtctggggcc aaggggaccac ggtcaccgtc tcctcagggtg gtggtggttc tggcggcggc   1140
ggctccggtg gtggtggttc tgagctcgtg atgaccacaga ctccactctc cctgcctgtc   1200
agtcttgagg atcaagcctc catctcttgc agatctagtc agagccttgt acacagtaat   1260
ggaaacacct atttacattg gtacctgcag aagccaggcc agtctccaaa gctcctgata   1320
taciaagttt ccaaccgatt ttctggggtc ccagacaggt tcagtggcag tggatcaggg   1380
acagatttca cactcaagat cagcagagtg gaggtgagg atctgggagt ttatttctgc   1440
tctcaaagta cacatgttcc gtacacgttc ggagggggga ccaagcttga gatcaaa    1497

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<210> 295

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> VL3/VH5x4-7 LHHL

<400> 295

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Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1           5           10           15

```

```

Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
20           25           30

```

```

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35           40           45

```

```

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50           55           60

```

```

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65           70           75           80

```

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe
180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr
210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser
245 250 255

Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys
260 265 270

Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln
275 280 285

Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile
290 295 300

Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr

<220>
<223> VH5VL3x4-7 HLHL

<400> 296

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cctggacagg gtctggaatg gattggatac attaataccta gccgtgggta tactaattac 180
gcagacagcg tcaagggccg cttcacaaac actacagaca aatccaccag cacagcctac 240
atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
gaaggtacta gtactggttc tgggtggaagt ggaggttcag gtggagcaga cgacattgta 420
ctgaccaggt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgacctgc 480
agagccagtt caagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcacc 540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccttgctcg cttcagtggc 600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
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aactatggtt taagctgggt gaagcagagg cctggacagg tccttgagtg gattggagag 900
gtttatccta gaattggtta tgcttactac aatgagaagt tcaagggcaa ggccacactg 960
actgcagaca aatcctocag cacagcgtcc atggagctcc gcagcctgac ctctgaggac 1020
tctgcggtct atttctgtgc aagacgggga tcctacgata ctaactacga ctggtacttc 1080
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gtcagtcttg gagatcaagc ctccatctct tgcagatcta gtcagagcct tgtacacagt 1260
aatggaaaca cctatttaca ttggtacctg cagaagccag gccagtctcc aaagctcctg 1320
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gggacagatt tcacactcaa gatcagcaga gtggaggctg aggatctggg agtttatttc 1440
tgctctcaaa gtacacatgt tccgtacag ttccggaggg ggaccaagct tgagatcaaa 1500
cat 1503

<210> 297

<211> 500

<212> PRT

<213> artificial sequence

<220>

<223> VH5VL3x4-7 HLHL

<400> 297

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
 145 150 155 160

Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln
 245 250 255

Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys
 260 265 270

Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys
 275 280 285

Gln Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg
 290 295 300

Ile Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu
 305 310 315 320

Thr Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu
 325 330 335

Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr
 340 345 350

Asp Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr
 355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380

Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu Pro
 385 390 395 400

Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
 405 410 415

Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys
 420 425 430

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
 435 440 445

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe

450

455

460

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe
 465 470 475 480

Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys
 485 490 495

Leu Glu Ile Lys
 500

<210> 298

<211> 1497

<212> DNA

<213> artificial sequence

<220>

<223> VL3VH5x4-7 LHLH

<400> 298

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 aaggcaccca aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
 ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
 gatgctgccca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cgggtggcggg 300
 accaagggtgg agatcaaagg cgaagggtact agtactgggt ctggtggaag tggaggttca 360
 ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
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 gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggt 540
 tatactaatt acgcagacag cgtcaagggc cgcttcacia tctactacaga caaatccacc 600
 agcacagcct acatggaact gagcagcctg cgttctgagg aactgcaac ctattactgt 660
 gcaagatatt atgatgatca ttactgcctt gactactggg gccaaggcac cacggtcacc 720
 gtctctctcg gaggtggtgg atccgagctc gtgatgacct agactccact ctccctgcct 780
 gtcagtcttg gagatcaagc ctccatctct tgcagatcta gtcagagcct tgtacacagt 840
 aatggaaaca cctatttaca ttgggtacctg cagaagccag gccagtctcc aaagctcctg 900
 atctacaaag tttccaaccg attttctggg gtcccagaca ggttcagtgg cagtggatca 960
 gggacagatt tcacactcaa gatcagcaga gtggaggctg aggatctggg agttttatttc 1020
 tgctctcaaa gtacacatgt tccgtacacg ttcggagggg ggaccaagct tgagatcaaa 1080


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gagcagtctg gagctgagct ggcgaggcct ggggcttcag tgaagctgtc ctgcaaggct 1200
tctggctaca ccttcacaaa ctatggttta agctgggtga agcagaggcc tggacaggtc 1260
cttgagtgga ttggagaggt ttatcctaga attggtaatg cttactacaa tgagaagttc 1320
aagggaagg ccacactgac tgcagacaaa tcctccagca cagcgtccat ggagctccgc 1380
agcctgacct ctgaggactc tgcggtctat ttctgtgcaa gacggggatc ctacgatact 1440
aactacgact ggtacttcga tgtctggggc caagggacca cggtcaccgt ctctca 1497

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<210> 299

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> VL3/VH5x4-7 LHLH

<400> 299

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Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1           5           10           15

```

```

Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
20           25           30

```

```

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35           40           45

```

```

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50           55           60

```

```

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65           70           75           80

```

```

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85           90           95

```

```

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
100          105          110

```

```

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
115          120          125

```

```

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val

```

130

135

140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
 145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe
 180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr
 210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro
 245 250 255

Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg
 260 265 270

Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp
 275 280 285

Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val
 290 295 300

Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser
 305 310 315 320

Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu
 325 330 335

Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly
 340 345 350

Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly
 355 360 365

Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser Gly
 370 375 380

Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala
 385 390 395 400

Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln Arg
 405 410 415

Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile Gly
 420 425 430

Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala
 435 440 445

Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr Ser
 450 455 460

Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp Thr
 465 470 475 480

Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val Thr
 485 490 495

Val Ser Ser

<210> 300
 <211> 1500
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH5VL3x4-7 HLLH

<400> 300
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 cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 180
 gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240
 atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc 360
 gaagggtacta gtactgggttc tgggtggaagt ggaggttcag gtggagcaga cgacattgta 420

ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgacctgc 480
 agagccagtt caagtgttaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
 acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaagggtg 720
 gagatcaaat ccggagggtg tggatccgag ctcgtgatga ccagactcc actctccctg 780
 cctgtcagtc ttggagatca agcctccatc tcttgcatat ctagtcagag ccttgtagac 840
 agtaatggaa acacctatct acattggtac ctgcagaagc caggccagtc tccaaagctc 900
 ctgatctaca aagtttccaa ccgattttct ggggtcccag acagggttcag tggcagtggg 960
 tcagggacag atttcacact caagatcagc agagtggagg ctgaggatct gggagtttat 1020
 ttctgctctc aaagtacaca tgttccgtac acgttcggag gggggaccaa gcttgagatc 1080
 aaaggtggtg gtggttcttg cggcggcggc tccggtggtg gtggttctga ggtgcagctg 1140
 ctcgagcagt ctggagctga gctggcgagg cctggggctt cagtgaagct gtcctgcaag 1200
 gcttctggct acaccttcac aaactatggt ttaagctggg tgaagcagag gcctggacag 1260
 gtccttgagt ggattggaga ggtttatcct agaattggtg atgcttacta caatgagaag 1320
 ttcaagggca aggccacact gactgcagac aaatcctcca gcacagcgtc catggagctc 1380
 cgcagcctga cctctgagga ctctgcggtc tatttctgtg caagacgggg atcctacgat 1440
 actaactacg actggtactt cgatgtctgg ggccaaggga ccacggtcac cgtctcctca 1500

<210> 301

<211> 500

<212> PRT

<213> artificial sequence

<220>

<223> VH5VL3x4-7 HLLH

<400> 301

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
145 150 155 160

Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr
245 250 255

Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys
260 265 270

Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His
275 280 285

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys
 290 295 300

Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
 305 310 315 320

Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp
 325 330 335

Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe
 340 345 350

Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly
 355 360 365

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser
 370 375 380

Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys
 385 390 395 400

Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln
 405 410 415

Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile
 420 425 430

Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr
 435 440 445

Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr
 450 455 460

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp
 465 470 475 480

Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val
 485 490 495

Thr Val Ser Ser
 500

<210> 302
 <211> 1497

<212> DNA

<213> artificial sequence

<220>

<223> VL1VH7x4-7 LHHL

<400> 302

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atcacctgca gagccagtc aagtgttaagt tacatgaact ggtaccagca gaagccgggc	120
aaggcaccca aaagatggat ttatgacaca tccaaagtgg cttctggagt cctgtctgc	180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa	240
gatgctgcc a ttattactg ccaacagtgg agtagtaacc cgctcacgtt cgggtggcggg	300
accaagggtg agatcaaagg cgaagggtact agtactgggt ctggtggaag tggagggttca	360
ggtggagcag acgagctcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc	420
tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg	480
gtaaggcagg cacctggaca ggggtctggaa tggattggat acattaatcc tagccgtgg	540
tatactaatt acaatcagaa gttcaaggac cgcgtcacia tctactacaga caaatccacc	600
agcacagcct acatggaact gagcagcctg cgttctgagg aactgcagt ctattactgt	660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac caggttcacc	720
gtctctccg gaggtggtg atccgaggtg cagctgctcg agcagtctgg agctgagctg	780
gcgaggcctg gggcttcagt gaagctgtcc tgcaaggctt ctggctacac cttcaciaaac	840
tatggtttaa gctgggtgaa gcagaggcct ggacaggctc ttgagtggat tggagagggt	900
tatcctagaa ttggtaatgc ttactacaat gagaagttca agggcaaggc cacactgact	960
gcagacaaat cctccagcac agcgtccatg gagctccgca gcctgacctc tgaggactct	1020
gcggtctatt tctgtgcaag acgggggatcc tacgatacta actacgactg gtacttcgat	1080
gtctggggcc aagggaaccac ggtcaccgtc tcctcaggtg gtggtggttc tggcggcggc	1140
ggctccggtg gtggtggttc tgagctcgtg atgaccaga ctccactctc cctgcctgtc	1200
agtcttgag atcaagcctc catctcttgc agatctagtc agagccttgt acacagtaat	1260
ggaaacacct atttacattg gtacctgcag aagccaggcc agtctccaaa gctcctgatc	1320
tacaaagttt ccaaccgatt ttctggggtc ccagacaggt tcagtggcag tggatcaggg	1380
acagatttca cactcaagat cagcagagtg gaggctgagg atctgggagt ttatttctgc	1440
tctcaaagta cacatgttcc gtacacgttc ggagggggga ccaagcttga gatcaaa	1497

<210> 303

<211> 499
<212> PRT
<213> artificial sequence

<220>
<223> VL1VH7x4-7 LHHL

<400> 303

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr
 210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser
 245 250 255

Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys
 260 265 270

Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln
 275 280 285

Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile
 290 295 300

Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr
 305 310 315 320

Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr
 325 330 335

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp
 340 345 350

Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val
 385 390 395 400

Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
 405 410 415

Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
 420 425 430

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser

435

440

445

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 450 455 460

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
 465 470 475 480

Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
 485 490 495

Glu Ile Lys

<210> 304
 <211> 1500
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH7-VL1x4-7 HLHL

<400> 304
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 cctggacagg gtctggaatg gattggatac attaactcta gccgtgggta tactaattac 180
 aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac 240
 atggaactga gcagcctgog ttctgaggac actgcagtct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctccctcaggc 360
 gaagg tacta gtactgggtc tgggtggaagt ggagggtcag gtggagcaga cgacattcag 420
 atgacccagt ctccatctag cctgtctgca tctgtcgggg accgtgtcac catcacctgc 480
 agagccagtc aaagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tccttgctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
 acttattact gccaacagtg gagtagtaac ccgctcacgt tcgggtggcg gaccaaggtg 720
 gagatcaa at ccggagggtg tggatccgag gtgcagctgc tcgagcagtc tggagctgag 780
 ctggcgaggc ctggggcttc agtgaagctg tcctgcaagg cttctggcta caccttcaca 840
 aactatgggt taagctgggt gaagcagagg cctggacagg tccttgagtg gattggagag 900
 gtttatccta gaattggtaa tgcttactac aatgagaagt tcaagggcaa ggccacactg 960

actgcagaca aatcctccag cacagcgtcc atggagctcc gcagcctgac ctctgaggac 1020
 tctgcggtct atttctgtgc aagacgggga tcctacgata ctaactacga ctggtacttc 1080
 gatgtctggg gccaaaggac cacggtcacc gtctcctcag gtggtggtgg ttctggcggc 1140
 ggcggctccg gtggtggtgg ttctgagctc gtgatgaccc agactccact ctccctgcct 1200
 gtcagtcttg gagatcaagc ctccatctct tgcagatcta gtcagagcct tgtacacagt 1260
 aatggaaaca cctattttaca ttggtacctg cagaagccag gccagtctcc aaagctcctg 1320
 atctacaaag tttccaaccg attttctggg gtcccagaca ggttcagtgg cagtggatca 1380
 gggacagatt tcacactcaa gatcagcaga gtggaggctg aggatctggg agtttatttc 1440
 tgctctcaaa gtacacatgt tccgtacacg ttccggagggg ggaccaagct tgagatcaaa 1500

<210> 305
 <211> 500
 <212> PRT
 <213> artificial sequence

<220>
 <223> VH7-VL1x4-7 HLHL

<400> 305

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
 50 55 60

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly

115

120

125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser
 130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
 145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln
 245 250 255

Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys
 260 265 270

Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys
 275 280 285

Gln Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg
 290 295 300

Ile Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu
 305 310 315 320

Thr Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu
 325 330 335

Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr
 340 345 350

Asp Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr
 355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380

Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu Pro
 385 390 395 400

Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
 405 410 415

Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys
 420 425 430

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
 435 440 445

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
 450 455 460

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe
 465 470 475 480

Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys
 485 490 495

Leu Glu Ile Lys
 500

<210> 306

<211> 1497

<212> DNA

<213> artificial sequence

<220>

<223> VL1-VH7x4-7 LHLH

<400> 306

gacattcaga tgaccacagtc tccatctagc ctgtctgcat ctgtcgggga cagtgtcacc 60

atcacctgca gagccagtc aagtgttaagt tacatgaact ggtaccagca gaagccgggc 120

aaggcaccga aaagatggat ttatgacaca tccaaagtgg cttctggagt cctgtctgcg 180

ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240

gatgctgcc aattattactg ccaacagtgg agtagtaacc cgctcacgtt cgggtggcggg 300

accaagggtgg agatcaaagg cgaagggtact agtactgggtt ctggtggaag tggagggttca 360
 ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctgggggcc 420
 tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
 gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggt 540
 tatactaatt acaatcagaa gttcaaggac cgcgtcacia tctactacaga caaatccacc 600
 agcacagcct acatggaact gagcagcctg cggttctgagg aactgcagt ctattactgt 660
 gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc 720
 gtctctctcg gaggtggtgg atccgagctc gtgatgaccc agactccact ctccctgcct 780
 gtcagtcttg gagatcaagc ctccatctct tgcagatcta gtcagagcct tgtacacagt 840
 aatggaaaca cctatttaca ttggtacctg cagaagccag gccagtctcc aaagctectg 900
 atctacaaag tttccaaccg attttctggg gtcccagaca gggttcagtgg cagtggatca 960
 gggacagatt tcacactcaa gatcagcaga gtggaggctg aggatctggg agtttatttc 1020
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 ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctgaggt gcagctgctc 1140
 gagcagtctg gagctgagct ggcgaggcct ggggcttcag tgaagctgtc ctgcaaggct 1200
 tctggctaca cttcacaaa ctatggttta agctgggtga agcagaggcc tggacaggtc 1260
 cttgagtgga ttggagaggt ttatcctaga attggtaatg cttactacaa tgagaagttc 1320
 aagggcaagg ccacactgac tgcagacaaa tcctccagca cagcgtccat ggagctccgc 1380
 agcctgacct ctgaggactc tgcggtctat ttctgtgcaa gacggggatc ctacgatact 1440
 aactacgact ggtacttcga tgtctggggc caagggacca cggtcaccgt ctctca 1497

<210> 307

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> VL1-VH7x4-7 LHLH

<400> 307

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
 20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
 35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
 100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
 115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
 145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
 180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr
 210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro
 245 250 255

Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg
 260 265 270

Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp
 275 280 285

Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val
 290 295 300

Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser
 305 310 315 320

Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu
 325 330 335

Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly
 340 345 350

Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly
 355 360 365

Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser Gly
 370 375 380

Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala
 385 390 395 400

Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln Arg
 405 410 415

Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile Gly
 420 425 430

Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala
 435 440 445

Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr Ser
 450 455 460

Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp Thr
 465 470 475 480

Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val Thr
 485 490 495

Val Ser Ser

<210> 308
 <211> 1500
 <212> DNA
 <213> artificial sequence

<220>

<223> VH7-VL1x4-7 HLLH

<400> 308

gacgtccaac tggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg	60
tcctgcaagg cttctggcta cacctttact aggtacacga tgactgggt aaggcaggca	120
cctggacagg gtctggaatg gattggatac attaattccta gccgtgggta tactaattac	180
aatcagaagt tcaaggaccg cgtcaccaatc actacagaca aatccaccag cacagcctac	240
atggaactga gcagcctgag ttctgaggac actgcagtct attactgtgc aagatattat	300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc	360
gaagggtacta gtactgggtc tggtggaagt ggagggtcag gtggagcaga cgacattcag	420
atgaccagct ctccatctag cctgtctgca tctgtcgggg accgtgtcac catcacctgc	480
agagccagtc aaagtgtgaa ttacatgaac tggtaccagc agaagccggg caaggcaccc	540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc	600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc	660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcgggtggcg gaccaagggtg	720
gagatcaaat ccggagggtg tggtaccgag ctctgtgatga ccagactcc actctccctg	780
cctgtcagtc ttggagatca agcctccatc tcttgagat ctagtcagag ccttgtagac	840
agtaatggaa acacctatctt acattgggtac ctgcagaagc caggccagtc tccaaagctc	900
ctgatctaca aagtttccaa ccgattttct ggggtcccag acagggtcag tggcagtggg	960
tcagggacag atttcacact caagatcagc agagtggagg ctgaggatct gggagtttat	1020
ttctgctctc aaagtacaca tgttccgtac acgttcggag gggggaccaa gcttgagatc	1080
aaagggtggtg gtggttctgg cggcgggcggc tccggtggtg gtggttctga ggtgcagctg	1140
ctcgagcagt ctggagctga gctggcgagg cctggggctt cagtgaagct gtcctgcaag	1200
gcttctggct acaccttcac aaactatggt ttaagctggg tgaagcagag gcctggacag	1260
gtccttgagt ggattggaga ggtttatcct agaattggta atgcttacta caatgagaag	1320
ttcaagggca agggcacact gactgcagac aaatcctcca gcacagcgtc catggagctc	1380
cgcagcctga cctctgagga ctctgcggtc tatttctgtg caagacgggg atcctacgat	1440

actaactacg actggtactt cgatgtctgg ggccaaggga ccacggtcac cgtctcctca 1500

<210> 309

<211> 500

<212> PRT

<213> artificial sequence

<220>

<223> VH7-VL1x4-7 HLLH

<400> 309

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser
130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr
 245 250 255

Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys
 260 265 270

Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His
 275 280 285

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys
 290 295 300

Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
 305 310 315 320

Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp
 325 330 335

Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe
 340 345 350

Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly
 355 360 365

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser
 370 375 380

Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys
 385 390 395 400

Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln
 405 410 415

Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile

420 425 430

Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr
 435 440 445

Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr
 450 455 460

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp
 465 470 475 480

Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val
 485 490 495

Thr Val Ser Ser
 500

<210> 310
 <211> 1497
 <212> DNA
 <213> artificial sequence

<220>
 <223> VL2VH7x4-7 LHL

<400> 310
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 ctgagctgca gagccagtc aagtgttaagt tacatgaact ggtaccagca gaagccgggc 120
 aaggcaccga aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
 ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
 gatgctgcca ottattactg ccaacagtgg agtagtaacc cgctcacgtt cgggtggcggg 300
 accaaggtgg agatcaaagg cgaaggtact agtactgggt ctggtggaag tggaggttca 360
 ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
 tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
 gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggt 540
 tatactaatt acaatcagaa gttcaaggac cgcgtcacia tcaactacaga caaatccacc 600
 agcacagcct acatggaact gagcagcctg cgttctgagg aactgcagt ctattactgt 660
 gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc 720
 gtctcctccg gaggtggtgg atccgaggtg cagctgctcg agcagtctgg agctgagctg 780
 gcgaggcctg gggcttcagt gaagctgtcc tgcaaggctt ctggctacac cttcaciaaac 840

tatgggtttaa gctgggtgaa gcagaggcct ggacagggtcc ttgagtggat tggagaggtt 900
 tatictagaa ttggtaatgc ttactacaat gagaagttca agggcaaggc cacactgact 960
 gcagacaaat cctccagcac agcgtccatg gagctccgca gcctgacctc tgaggactct 1020
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 gtctggggcc aagggaccac ggtcaccgtc tcctcagggtg gtggtggttc tggcggcggc 1140
 ggctccggtg gtggtggttc tgagctcgtg atgaccaga ctccactctc cctgcctgtc 1200
 agtcttgag atcaagcctc catctcttgc agatctagtc agagccttgt acacagtaat 1260
 ggaaacacct atttacattg gtacctgcag aagccaggcc agtctccaaa gctcctgatc 1320
 tacaaagttt ccaaccgatt ttctggggtc ccagacaggt tcagtggcag tggatcaggg 1380
 acagatttca cactcaagat cagcagagtg gaggtgagg atctgggagt ttatttctgc 1440
 tctcaaagta cacatgttcc gtacacgttc ggagggggga ccaagcttga gatcaaa 1497

<210> 311
 <211> 499
 <212> PRT
 <213> artificial sequence

<220>
 <223> VL2VH7x4-7 LHHL

<400> 311

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
 20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
 35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr

100	105	110
Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu		
115	120	125
Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val		
130	135	140
Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp		
145	150	155
Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn		
165	170	175
Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val		
180	185	190
Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser		
195	200	205
Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr		
210	215	220
Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr		
225	230	235
Val Ser Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser		
245	250	255
Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys		
260	265	270
Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln		
275	280	285
Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile		
290	295	300
Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr		
305	310	315
Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr		
325	330	335

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp
 340 345 350

Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val
 385 390 395 400

Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
 405 410 415

Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
 420 425 430

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
 435 440 445

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 450 455 460

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
 465 470 475 480

Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
 485 490 495

Glu Ile Lys

<210> 312

<211> 1500

<212> DNA

<213> artificial sequence

<220>

<223> VH7VL2x4-7 HLHL

<400> 312

gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaaggtg 60

tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120

cctggacagg gtctggaatg gattggatac attaataccta gccgtgggta tactaattac 180

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aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac   240
atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat   300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctccctcaggc   360
gaaggtacta gtactggttc tgggtggaagt ggaggttcag gtggagcaga cgacattgta   420
ctgaccagct ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc   480
agagccagtc aaagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc   540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc   600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc   660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg   720
gagatcaaat ccggagggtg tggatccgag gtgcagctgc tcgagcagtc tggagctgag   780
ctggcgaggc ctggggcttc agtgaagctg tcctgcaagg cttctggcta caccttcaca   840
aactatggtt taagctgggt gaagcagagg cctggacagg tccttgagtg gattggagag   900
gtttatccta gaattggtaa tgcttactac aatgagaagt tcaagggcaa ggccacactg   960
actgcagaca aatcctccag cacagcgtcc atggagctcc gcagcctgac ctctgaggac  1020
tctgcggtct atttctgtgc aagacgggga tcctacgata ctaactacga ctggtacttc  1080
gatgtctggg gccaaaggac cacggtcacc gtctcctcag gtggtggtgg ttctggcggc  1140
ggcggctccg gtggtggtgg ttctgagctc gtgatgacc agactccact ctccctgcct  1200
gtcagtcttg gagatcaagc ctccatctct tgcagatcta gtcagagcct tgtacacagt  1260
aatggaaaca cctattttaca ttggtacctg cagaagccag gccagtctcc aaagctcctg  1320
atctacaaag tttccaaccg attttctggg gtcccagaca ggttcagtgg cagtggatca  1380
gggacagatt tcacactcaa gatcagcaga gtggaggctg aggatctggg agtttatttc  1440
tgctctcaaa gtacacatgt tccgtacagc ttcggagggg ggaccaagct tgagatcaaa  1500

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<210> 313
<211> 500
<212> PRT
<213> artificial sequence

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<220>
<223> VH7VL2x4-7 HLHL
<400> 313

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Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1           5           10           15

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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30
 Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
 50 55 60
 Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125
 Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140
 Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 145 150 155 160
 Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175
 Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190
 Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205
 Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220
 Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240
 Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln
 245 250 255

Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys
 260 265 270

Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys
 275 280 285

Gln Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg
 290 295 300

Ile Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu
 305 310 315 320

Thr Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu
 325 330 335

Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr
 340 345 350

Asp Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr
 355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380

Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu Pro
 385 390 395 400

Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
 405 410 415

Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys
 420 425 430

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
 435 440 445

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
 450 455 460

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe
 465 470 475 480

Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys
 485 490 495

Leu Glu Ile Lys
500

<210> 314

<211> 1497

<212> DNA

<213> artificial sequence

<220>

<223> VL2VH7x4-7 LHLH

<400> 314

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aaggcaccca aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctgc	180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa	240
gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cgggtggcggg	300
accaaggtgg agatcaaagg cgaaggtact agtactgggt ctgggtggaag tggaggttca	360
ggtggagcag acgacgtcca actgggtgcag tcaggggctg aagtgaiaaaa acctggggcc	420
tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg	480
gtaaggcagg cacctggaca ggggtctggaa tggattggat acattaatcc tagccgtgg	540
tatactaatt acaatcagaa gttcaaggac cgcgtcacia tcactacaga caaatccacc	600
agcacagcct acatggaact gagcagcctg cggtctgagg aactgcagt ctattactgt	660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggac cacggtcacc	720
gtctcctccg gaggtggtgg atccgagctc gtgatgacct agactccact ctccctgcct	780
gtcagtcttg gagatcaagc ctccatctct tgcagatcta gtcagagcct tgtacacagt	840
aatggaaaca cctattttaca ttggtacctg cagaagccag gccagtctcc aaagctcctg	900
atctacaaag tttccaaccg attttctggg gtcccagaca ggttcagtgg cagtggatca	960
gggacagatt tcacactcaa gatcagcaga gtggaggctg aggatctggg agttttatttc	1020
tgctctcaaa gtacacatgt tccgtacacg ttcggagggg ggaccaagct tgagatcaaa	1080
ggtggtggtg gttctggcgg cggcggtctc ggtggtggtg gttctgaggt gcagctgctc	1140
gagcagtctg gagctgagct ggcgaggcct ggggcttcag tgaagctgtc ctgcaaggct	1200
tctggctaca ccttcacaaa ctatggttta agctgggtga agcagaggcc tggacaggct	1260
cttgagtgga ttggagaggt ttatcctaga attggtaatg ctactacaa tgagaagttc	1320

aagggcaagg ccacactgac tgcagacaaa tcctccagca cagcgtccat ggagctccgc 1380

agcctgacct ctgaggactc tgcggtctat ttctgtgcaa gacggggatc ctacgatact 1440

aactacgact ggtacttcga tgtctggggc caagggacca cggtcaccgt ctctca 1497

<210> 315

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> VL2VH7x4-7 LHLH

<400> 315

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
 180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr
 210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro
 245 250 255

Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg
 260 265 270

Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp
 275 280 285

Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val
 290 295 300

Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser
 305 310 315 320

Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu
 325 330 335

Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly
 340 345 350

Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly
 355 360 365

Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser Gly
 370 375 380

Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala
 385 390 395 400

Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln Arg

405

410

415

Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile Gly
 420 425 430

Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala
 435 440 445

Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr Ser
 450 455 460

Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp Thr
 465 470 475 480

Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val Thr
 485 490 495

Val Ser Ser

<210> 316

<211> 1500

<212> DNA

<213> artificial sequence

<220>

<223> VH7VL2x4-7 HLLH

<400> 316

gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg 60
 tcttgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120
 cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 180
 aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac 240
 atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
 gaagggtacta gtactgggtc tgggtggaagt ggagggttcag gtggagcaga cgacattgta 420
 ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480
 agagccagtc aaagtgtgaa ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
 acttattact gccaacagtg gagtagtaac ccgctcacgt tcgggtggcgg gaccaagggtg 720

gagatcaaat ccggaggtgg tggatccgag ctctgatga ccagactcc actctccctg 780
 cctgtcagtc ttggagatca agcctccatc tcttgagat ctagtcagag ccttgtagac 840
 agtaatggaa acacctatctt acattggtac ctgcagaagc caggccagtc tccaaagctc 900
 ctgatctaca aagtttccaa ccgattttct ggggtcccag acaggttcag tggcagtgga 960
 tcagggacag atttcacact caagatcagc agagtggagg ctgaggatct gggagtttat 1020
 ttctgctctc aaagtagaca tgttccgtac acgttcggag gggggaccaa gcttgagatc 1080
 aaaggtggtg gtggttctgg cggcggcggc tccggtggtg gtggttctga ggtgcagctg 1140
 ctcgagcagt ctggagctga gctggcgagg cctggggctt cagtgaagct gtcctgcaag 1200
 gcttctggct acaccttcac aaactatggt ttaagctggg tgaagcagag gcctggacag 1260
 gtccttgagt ggattggaga ggtttatcct agaattggta atgcttacta caatgagaag 1320
 ttcaagggca aggccacact gactgcagac aaatcctcca gcacagcgtc catggagctc 1380
 cgcagcctga cctctgagga ctctgcggtc tatttctgtg caagacgggg atcctacgat 1440
 actaactacg actggtactt cgatgtctgg ggccaaggga ccacggtcac cgtctcctca 1500

<210> 317

<211> 500

<212> PRT

<213> artificial sequence

<220>

<223> VH7VL2x4-7 HLLH

<400> 317

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
 50 55 60

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr
 245 250 255

Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys
 260 265 270

Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His
 275 280 285

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys
 290 295 300

Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
 305 310 315 320

Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp
 325 330 335

Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe
 340 345 350

Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly
 355 360 365

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser
 370 375 380

Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys
 385 390 395 400

Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln
 405 410 415

Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile
 420 425 430

Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr
 435 440 445

Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr
 450 455 460

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp
 465 470 475 480

Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val
 485 490 495

Thr Val Ser Ser
 500

<210> 318
 <211> 1497
 <212> DNA
 <213> artificial sequence

<220>
 <223> VL3VH7x4-7 LHHL

<400> 318
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ctgacctgca gagccagttc aagtgttaagt tacatgaact ggtaccagca gaagccgggc 120
aaggcaccca aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
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acagatttca cactcaagat cagcagagtg gaggctgagg atctgggagt ttatttctgc 1440
tctcaaagta cacatgttcc gtacacgttc ggagggggga ccaagcttga gatcaaa 1497

<210> 319

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> VL3VH7x4-7 LHHL

<400> 319

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr
210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser
 245 250 255

Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys
 260 265 270

Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln
 275 280 285

Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile
 290 295 300

Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr
 305 310 315 320

Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr
 325 330 335

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp
 340 345 350

Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val
 385 390 395 400

Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
 405 410 415

Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
 420 425 430

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
 435 440 445

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 450 455 460

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
 465 470 475 480

Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
 485 490 495

Glu Ile Lys

<210> 320
 <211> 1500
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH7VL3x4-7 HLHL

<400> 320
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 cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 180
 aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac 240
 atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
 gaaggtacta gtactggttc tgggtggaagt ggaggttcag gtggagcaga cgacattgta 420
 ctgaccaggt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgacctgc 480
 agagccagtt caagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tccttgctcg cttcagtggc 600
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 gagatcaaat ccggaggtgg tggatccgag gtgcagctgc tcgagcagtc tggagctgag 780
 ctggcgaggc ctggggcttc agtgaagctg tcctgcaagg cttctggcta caccttcaca 840
 aactatggtt taagctgggt gaagcagagg cctggacagg tccttgagtg gattggagag 900
 gtttatccta gaattggtaa tgcttactac aatgagaagt tcaagggcaa ggccacactg 960
 actgcagaca aatcctccag cacagcgtcc atggagctcc gcagcctgac ctctgaggac 1020
 tctgcggtct atttctgtgc aagacgggga tcctacgata ctaactacga ctggtacttc 1080
 gatgtctggg gccaaaggac cacggtcacc gtctcctcag gtggtggtgg ttctggcggc 1140
 ggcggtccg gtggtggtgg ttctgagctc gtgatgacct agactccact ctccctgcct 1200

gtcagtcttg gagatcaagc ctccatctct tgcagatcta gtcagagcct tgtacacagt 1260
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gggacagatt tcacactcaa gatcagcaga gtggaggctg aggatctggg agttttatttc 1440
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<210> 321
<211> 500
<212> PRT
<213> artificial sequence

<220>
<223> VH7VL3x4-7 HLHL

<400> 321

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
145 150 155 160

Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln
 245 250 255

Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys
 260 265 270

Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys
 275 280 285

Gln Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg
 290 295 300

Ile Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu
 305 310 315 320

Thr Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu
 325 330 335

Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr
 340 345 350

Asp Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr
 355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380

Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu Pro

385 390 395 400

Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
 405 410 415

Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys
 420 425 430

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
 435 440 445

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
 450 455 460

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe
465 470 475 480

Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys
 485 490 495

Leu Glu Ile Lys
 500

<210> 322
<211> 1497
<212> DNA
<213> artificial sequence

<220>
<223> VL3VH7x4-7 LHLH

<400> 322
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aaggcaccga aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
gatgctgcca ottattactg ccaacagtgg agtagtaacc cgctcacgtt cggtggcggg 300
accaaggtgg agatcaaagg cgaaggtact agtactggtt ctggtggaag tggaggttca 360
gggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggg 540
tatactaatt acaatcagaa gttcaaggac cgcgtcacia tctactacaga caaatccacc 600


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agcacagcct acatggaact gagcagcctg cgttctgagg aactgcagt ctattactgt    660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc    720
gtctcctccg gaggtggtgg atccgagctc gtgatgaccc agactccact ctcctgcct    780
gtcagtcctt gagatcaagc ctccatctct tgcagatcta gtcagagcct tgtacacagt    840
aatggaaca cctatttaca ttggtacctg cagaagccag gccagtctcc aaagctcctg    900
atctacaaag tttccaaccg attttctggg gtcccagaca ggttcagtgg cagtggatca    960
gggacagatt tcacactcaa gatcagcaga gtggaggctg aggatctggg agtttatctc   1020
tgctctcaaa gtaacatgt tccgtacacg ttcggagggg ggaccaagct tgagatcaaa   1080
ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctgaggt gcagctgctc   1140
gagcagtctg gagctgagct ggcgaggcct ggggcttcag tgaagctgtc ctgcaaggct   1200
tctggctaca ccttcacaaa ctatggttta agctgggtga agcagaggcc tggacaggctc   1260
cttgagtgga ttggagaggt ttatcctaga attggtaatg ctactacaa tgagaagttc   1320
aagggcaagg ccacactgac tgcagacaaa tcctccagca cagcgtccat ggagctccgc   1380
agcctgacct ctgaggactc tgcggtctat ttctgtgcaa gacggggatc ctacgatact   1440
aactacgact ggtacttcga tgtctggggc caagggacca cggtcaccgt ctcctca    1497

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<210> 323

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> VL3VH7x4-7 LHLH

<400> 323

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Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1           5           10           15

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Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
          20           25           30

```

```

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35           40           45

```

```

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50           55           60

```

```

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu

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65		70		75		80									
Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Ser	Asn	Pro	Leu	Thr
			85						90					95	
Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Gly	Glu	Gly	Thr	Ser	Thr
			100					105					110		
Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ala	Asp	Asp	Val	Gln	Leu
		115					120					125			
Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val
	130					135					140				
Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Arg	Tyr	Thr	Met	His	Trp
145					150					155					160
Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Asn
				165					170					175	
Pro	Ser	Arg	Gly	Tyr	Thr	Asn	Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Arg	Val
			180					185					190		
Thr	Ile	Thr	Thr	Asp	Lys	Ser	Thr	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Ser
		195					200					205			
Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Tyr	Tyr
	210					215					220				
Asp	Asp	His	Tyr	Cys	Leu	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr
225					230					235					240
Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Leu	Val	Met	Thr	Gln	Thr	Pro
			245						250					255	
Leu	Ser	Leu	Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg
			260					265					270		
Ser	Ser	Gln	Ser	Leu	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	His	Trp
		275					280					285			
Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val
	290					295					300				

Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser
 305 310 315 320

Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu
 325 330 335

Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly
 340 345 350

Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly
 355 360 365

Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser Gly
 370 375 380

Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala
 385 390 395 400

Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln Arg
 405 410 415

Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile Gly
 420 425 430

Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala
 435 440 445

Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr Ser
 450 455 460

Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp Thr
 465 470 475 480

Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val Thr
 485 490 495

Val Ser Ser

<210> 324
 <211> 1500
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH7VL3x4-7 HLLH

<400> 324
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cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 180
aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac 240
atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat 300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctccctcaggc 360
gaagggtacta gtactggttc tgggtggaagt ggagggttcag gtggagcaga cgacattgta 420
ctgaccagtc ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgacctgc 480
agagccagtt caagtgtgaa ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg 720
gagatcaaat ccggaggtgg tggatccgag ctctgtgatga cccagactcc actctccctg 780
cctgtcagtc ttggagatca agcctccatc tcttgcatg ctagtcagag ccttgtagac 840
agtaatggaa acacctatct acattgggtac ctgcagaagc caggccagtc tccaaagctc 900
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gcttctggct acaccttcac aaactatggt ttaagctggg tgaagcagag gcctggacag 1260
gtccctgagt ggattggaga ggtttatcct agaattggtg atgcttacta caatgagaag 1320
ttcaagggca aggccacact gactgcagac aaatcctcca gcacagcgtc catggagctc 1380
cgcagcctga cctctgagga ctctgcggtc tatttctgtg caagacgggg atcctacgat 1440
actaactacg actggtactt cgatgtctgg ggccaaggga ccacggtcac cgtctcctca 1500

<210> 325

<211> 500

<212> PRT

<213> artificial sequence

<220>

<223> VH7VL3x4-7 HLLH

<400> 325

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
 50 55 60

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
 145 150 155 160

Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Thr
 245 250 255

Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys
 260 265 270

Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His
 275 280 285

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys
 290 295 300

Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
 305 310 315 320

Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp
 325 330 335

Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe
 340 345 350

Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly
 355 360 365

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Gln Ser
 370 375 380

Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys
 385 390 395 400

Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu Ser Trp Val Lys Gln
 405 410 415

Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu Val Tyr Pro Arg Ile
 420 425 430

Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr
 435 440 445

Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Glu Leu Arg Ser Leu Thr
 450 455 460

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Ser Tyr Asp
 465 470 475 480

Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val
 485 490 495

Thr Val Ser Ser
 500

<210> 326

<211> 1494

<212> DNA

<213> artificial sequence

<220>

<223> VL1VH5xCD19 LHHL

<400> 326

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aaggcaccga aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc	180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa	240
gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cgggtggcggg	300
accaaggtgg agatcaaagg cgaaggtact agtactggtt ctggtggaag tggaggttca	360
ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc	420
tcagtgaagg tgtctctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg	480
gtaaggcagg cacctggaca ggggtctggaa tggattggat acattaatcc tagccgtggg	540
tatactaatt acgcagacag cgtcaagggc cgcttcacia tctactacaga caaatccacc	600
agcacagcct acatggaact gagcagcctg cgcttctgagg aactgcaac ctattactgt	660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac caccgtcacc	720
gtctcctccg gaggtggtgg atcccagggtg cagctgcagc agtctggggc tgagctggtg	780
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tggatgaact ggggtgaagca gaggcctgga cagggtcttg agtggattgg acagatttgg	900
cctggagatg gtgatactaa ctacaatgga aagttcaagg gtaaagccac tctgactgca	960
gacgaatcct ccagcacagc ctacatgcaa ctcagcagcc tagcatctga ggactctgcg	1020
gtctattttct gtgcaagacg ggagactacg acggtaggcc gttattacta tgctatggac	1080

tactggggcc aagggaccac ggtcaccgtc tcctccggtg gtggtggttc tggcggcggc 1140
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 tctctagggc agagggccac catctcctgc aaggccagcc aaagtgttga ttatgatggt 1260
 gatagttatt tgaactggta ccaacagatt ccaggacagc caccctaaact cctcatctat 1320
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 gattcaccc tcaacatcca tcctgtggag aagggtggatg ctgcaaccta tcaactgtcag 1440
 caaagtactg aggatccgtg gacgttcggt ggagggacca agctcgagat caaa 1494

<210> 327
 <211> 498
 <212> PRT
 <213> artificial sequence

<220>
 <223> VL1VH5xCD19 LHHL

<400> 327

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
 20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
 35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
 100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
 115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
 145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe
 180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr
 210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly
 245 250 255

Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala
 260 265 270

Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg
 275 280 285

Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly
 290 295 300

Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala
 305 310 315 320

Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser
 325 330 335

Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val
 340 345 350

Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

370

375

380

Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val
 385 390 395 400

Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val
 405 410 415

Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly
 420 425 430

Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly
 435 440 445

Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 450 455 460

Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln
 465 470 475 480

Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
 485 490 495

Ile Lys

<210> 328

<211> 1497

<212> DNA

<213> artificial sequence

<220>

<223> VH5VL1xCD19 HLHL

<400> 328

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 cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 180
 gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240
 atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
 gaagg tacta gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacattcag 420
 atgacccagt ctccatctag cctgtctgca tctgtcgggg accgtgtcac catcacctgc 480

agagccagtc aaagtgtaag ttacatgaac tggtagcagc agaagccggg caaggcaccc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
 acttattact gccaacagtg gagtagtaac ccgctcacgt tgggtggcgg gaccaaggtg 720
 gagatcaaat ccggaggtgg tggatcccag gtgcagctgc agcagtctgg ggctgagctg 780
 gtgaggcctg ggtcctcagt gaagatttcc tgcaaggctt ctggctatgc attcagtagc 840
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 tggcctggag atggtgatac taactacaat ggaaagttca agggtaaagc cactctgact 960
 gcagacgaat cctccagcac agcctacatg caactcagca gcctagcatc tgaggactct 1020
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 gtgtctctag ggcagagggc caccatctcc tgcaaggcca gccaaagtgt tgattatgat 1260
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 acagacttca ccctcaacat ccctcctgtg gagaaggtgg atgctgcaac ctatcactgt 1440
 cagcaaagta ctgaggatcc gtggacgttc ggtggaggga ccaagctcga gatcaaa 1497

<210> 329
 <211> 499
 <212> PRT
 <213> artificial sequence

<220>
 <223> VH5VL1xCD19 HLHL

<400> 329

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser
130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser
245 250 255

Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys
260 265 270

Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln
275 280 285

Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp
 290 295 300

Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr
 305 310 315 320

Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala
 325 330 335

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr
 340 345 350

Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr
 355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380

Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala
 385 390 395 400

Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser
 405 410 415

Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro
 420 425 430

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser
 435 440 445

Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 450 455 460

Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys
 465 470 475 480

Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
 485 490 495

Glu Ile Lys

<210> 330
 <211> 1494
 <212> DNA

<213> artificial sequence

<220>

<223> VL1VH5xCD19 LHLH

<400> 330

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aaggcaccga aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc      180
ttcagtggca gtgggtctgg gaccgactac tctctcaca tcaacagctt ggaggctgaa      240
gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cggtggcggg      300
accaaggtgg agatcaaagg cgaagg tact agtactggtt ctggtggaag tggagggttca      360
ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc      420
tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcaactg      480
gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggt      540
tatactaatt acgcagacag cgtcaagggc cgcttcacaa tctactacaga caaatccacc      600
agcacagcct acatggaact gagcagcctg cgcttctgagg aactgcaac ctattactgt      660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc      720
gtctcctccg gaggtggtgg atccgatatc cagctgaccc agtctccagc ttctttggct      780
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tatgatgcat ccaatctagt ttctgggata ccaccagggt ttagtggcag tgggtctggg      960
acagacttca ccctcaacat ccatcctgtg gagaagggtg atgctgcaac ctatcactgt     1020
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ggtggtggtt ctggcggcgg cggtccggt ggtggtggtt ctcagggtgca gctgcagcag     1140
tctggggctg agctggtgag gcctgggtcc tcagtgaaga tttcctgcaa ggcttctggc     1200
tatgcattca gtagctactg gatgaactgg gtgaagcaga ggcctggaca gggctctgag     1260
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aaagccactc tgactgcaga cgaatcctcc agcacagcct acatgcaact cagcagccta     1380
gcatctgagg actctgcggt ctatttctgt gcaagacggg agactacgac ggtaggccgt     1440
tattactatg ctatggacta ctggggccaa gggaccacgg tcaccgtctc ctcc           1494

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<210> 331

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> VL1VH5xCD19 LHLH

<400> 331

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
 20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
 35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
 100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
 115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
 145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe
 180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr
 210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro
 245 250 255

Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys
 260 265 270

Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr
 275 280 285

Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser
 290 295 300

Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly
 305 310 315 320

Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala
 325 330 335

Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly
 340 345 350

Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly
 355 360 365

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
 370 375 380

Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
 385 390 395 400

Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly
 405 410 415

Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr
 420 425 430

Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu
 435 440 445

Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp
 450 455 460

Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg
 465 470 475 480

Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
 485 490 495

Ser Ser

<210> 332
 <211> 1497
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH5VL1xCD19 HLLH

<400> 332
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 cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 180
 gcagacagcg tcaagggcgc cttcacaatc actacagaca aatccaccag cacagcctac 240
 atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
 gaagg tacta gtactggttc tgggtggaagt ggagggtcag gtggagcaga cgacattcag 420
 atgaccagtc ctccatctag cctgtctgca tctgtcgggg accgtgtcac catcacctgc 480
 agagccagtc aaagtgtgaa ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
 acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaagggtg 720
 gagatcaa at ccggagggtg tggatccgat atccagctga ccagctctcc agcttctttg 780
 gctgtgtctc tagggcagag ggccaccatc tcttgcaagg ccagccaaag tgttgattat 840
 gatgggtgata gttatttgaa ctggtaccaa cagattccag gacagccacc caaactcctc 900
 atctatgatg catccaatct agtttctggg atcccacca ggtttagtgg cagtgggtct 960

```

gggacagact tcaccctcaa catccatcct gtggagaagg tggatgctgc aacctatcac 1020
tgtcagcaaa gtactgagga tccgtggacg ttcggtggag ggaccaagct cgagatcaaa 1080
ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctcaggt gcagctgcag 1140
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ggctatgcat tcagtagcta ctggatgaac tgggtgaagc agaggcctgg acagggcttt 1260
gagtggattg gacagatttg gcctggagat ggtgatacta actacaatgg aaagttcaag 1320
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ctagcatctg aggactctgc ggtctatttc tgtgcaagac gggagactac gacggtaggc 1440
cgttattact atgctatgga ctactggggc caagggacca cggtcaccgt ctctcc 1497

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<210> 333
<211> 499
<212> PRT
<213> artificial sequence

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<220>
<223> VH5VL1xCD19 HLLH

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<400> 333

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Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1           5           10           15

```

```

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20           25           30

```

```

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35           40           45

```

```

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
50           55           60

```

```

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65           70           75           80

```

```

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85           90           95

```

```

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100           105           110

```

```

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115           120           125

```

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser
 130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
 145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser
 245 250 255

Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys
 260 265 270

Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp
 275 280 285

Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala
 290 295 300

Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser
 305 310 315 320

Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala
 325 330 335

Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly
 340 345 350

Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly

355

360

365

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala
 370 375 380

Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser
 385 390 395 400

Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro
 405 410 415

Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp
 420 425 430

Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp
 435 440 445

Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu
 450 455 460

Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly
 465 470 475 480

Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 485 490 495

Val Ser Ser

<210> 334

<211> 1494

<212> DNA

<213> artificial sequence

<220>

<223> VL2/VH5xCD19 LHHL

<400> 334

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 aaggcaccga aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
 ttcagtggca gtgggtctgg gaccgactac tctctcaca tcaacagctt ggaggctgaa 240
 gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cgggtggcggg 300
 accaaggtgg agatcaaagg cgaaggtact agtactggtt ctggtggaag tggaggttca 360

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ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaa acctggggcc 420
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gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggt 540
tatactaatt acgcagacag cgtcaagggc cgcttcacaa tcactacaga caaatccacc 600
agcacagcct acatggaact gagcagcctg cgttctgagg aactgcaac ctattactgt 660
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tctctagggc agagggccac catctcctgc aaggccagcc aaagtgttga ttatgatggt 1260
gatagttatt tgaactggta ccaacagatt ccaggacagc caccctaaact cctcatctat 1320
gatgcatcca atctagtttc tgggatccca cccaggttta gtggcagtgg gtctgggaca 1380
gacttcaccc tcaacatcca tctgtggag aagggtggat ctgcaacctc tcaactgtcag 1440
caaagtactg aggatccgtg gacgttcggt ggagggacca agctcgagat caaa 1494

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<210> 335

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> VL2/VH5xCD19 LHHL

<400> 335

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Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1           5           10           15

```

```

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
          20           25           30

```

```

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr

```

35

40

45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
 100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
 115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
 145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe
 180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr
 210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly
 245 250 255

Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala
 260 265 270

Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg
 275 280 285

Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly
 290 295 300

Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala
 305 310 315 320

Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser
 325 330 335

Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val
 340 345 350

Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val
 385 390 395 400

Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val
 405 410 415

Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly
 420 425 430

Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly
 435 440 445

Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 450 455 460

Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln
 465 470 475 480

Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
 485 490 495

Ile Lys

<210> 336
 <211> 1497
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH5VL2xCD19 HLHL

<400> 336
 gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaaggtg 60
 tcttgcaagg cttctggcta cacctttact aggtacacga tgactgggt aaggcaggca 120
 cctggacagg gtctggaatg gattggatac attaataccta gccgtgggta tactaattac 180
 gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240
 atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
 gaaggacta gtactggttc tgggtggaagt ggaggttcag gtggagcaga cgacattgta 420
 ctgaccagtc ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480
 agagccagtc aaagtgtgaa ttacatgaac tggtagcagc agaagccggg caaggcaccc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
 acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg 720
 gagatcaaat ccggaggtgg tggatcccag gtgcagctgc agcagtctgg ggctgagctg 780
 gtgaggcctg ggtcctcagt gaagatttcc tgcaaggctt ctggctatgc attcagtagc 840
 tactggatga actgggtgaa gcagaggcct ggacagggtc ttgagtggat tggacagatt 900
 tggcctggag atggtgatac taactacaat ggaaagttca agggtaaagc cactctgact 960
 gcagacgaat cctccagcac agcctacatg caactcagca gcctagcatc tgaggactct 1020
 gcggtctatt tctgtgcaag acgggagact acgacggtag gccgttatta ctatgctatg 1080
 gactactggg gccaaaggac cacggtcacc gtctcctccg gtggtggtgg ttctggcggc 1140
 ggcggctccg gtggtggtgg ttctgatata cagctgaccc agtctccagc ttctttggct 1200
 gtgtctctag ggcagagggc caccatctcc tgcaaggcca gccaaagtgt tgattatgat 1260
 ggtgatagtt atttgaactg gtaccaacag attccaggac agccacccaa actcctcatc 1320
 tatgatgcat ccaatctagt ttctgggata ccaccagggt ttagtggcag tgggtctggg 1380
 acagacttca ccctcaacat ccctcctgtg gagaaggtgg atgctgcaac ctatcactgt 1440
 cagcaaagta ctgaggatcc gtggacgttc ggtggaggga ccaagctcga gatcaaa 1497

<210> 337
 <211> 499
 <212> PRT
 <213> artificial sequence

<220>
 <223> VH5VL2xCD19 HLHL

<400> 337

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser
 245 250 255

Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys
 260 265 270

Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln
 275 280 285

Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp
 290 295 300

Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr
 305 310 315 320

Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala
 325 330 335

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr
 340 345 350

Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr
 355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380

Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala
 385 390 395 400

Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser
 405 410 415

Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro
 420 425 430

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser
 435 440 445

Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 450 455 460

Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys
 465 470 475 480

Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
 485 490 495

Glu Ile Lys

<210> 338
 <211> 1494
 <212> DNA
 <213> artificial sequence

<220>
 <223> VL2/VH5xCD19

<400> 338
 gacattgtac tgaccagtc tccagcaact ctgtctctgt ctccagggga gcgtgccacc 60
 ctgagctgca gagccagtca aagtgttaagt tacatgaact ggtaccagca gaagccgggc 120
 aaggcaccga aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
 ttcagtggca gtgggtctgg gaccgactac tctctcaca tcaacagctt ggaggctgaa 240
 gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cggtggcggg 300
 accaaggtgg agatcaaagg cgaaggtact agtactgggt ctggtggaag tggaggttca 360
 ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
 tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcaactg 480
 gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggt 540
 tatactaatt acgcagacag cgtcaagggc cgcttcacaa tcaactacaga caaatccacc 600
 agcacagcct acatggaact gagcagcctg cgcttctgagg aactgcaac ctattactgt 660
 gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc 720
 gtctcctccg gaggtggtgg atccgatatc cagctgaccc agtctccagc ttctttggtt 780
 gtgtctctag ggcagagggc caccatctcc tgcaaggcca gccaaagtgt tgattatgat 840

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ggtgatagtt atttgaactg gtaccaacag attccaggac agccacccaa actcctcatc   900
tatgatgcat ccaatctagt ttctgggatc ccaccagggt ttagtggcag tgggtctggg   960
acagacttca ccctcaacat ccatcctgtg gagaagggtg atgctgcaac ctatcactgt  1020
cagcaaagta ctgaggatcc gtggacgttc ggtggaggga ccaagctcga gatcaaaggt  1080
ggtggtggtt ctggcggcgg cggtccgggt ggtggtggtt ctcagggtga gctgcagcag  1140
tctggggctg agctggtgag gcctgggtcc tcagtgaaga tttcctgcaa ggcttctggc  1200
tatgcattca gtagctactg gatgaactgg gtgaagcaga ggcctggaca gggctcttgag  1260
tggattggac agatttggcc tggagatggt gatactaact acaatggaaa gttcaagggt  1320
aaagccactc tgactgcaga cgaatcctcc agcacagcct acatgcaact cagcagccta  1380
gcatctgagg actctgcggt ctatttctgt gcaagacggg agactacgac ggtaggccgt  1440
tattactatg ctatggacta ctggggccaa gggaccacgg tcaccgtctc ctcc       1494

```

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<210> 339
<211> 498
<212> PRT
<213> artificial sequence

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<220>
<223> VL2/VH5xCD19

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<400> 339

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Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1           5           10           15

```

```

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
20           25           30

```

```

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35           40           45

```

```

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50           55           60

```

```

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65           70           75           80

```

```

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85           90           95

```

```

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
100          105          110

```

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
 115 120 125
 Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 130 135 140
 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
 145 150 155 160
 Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 165 170 175
 Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe
 180 185 190
 Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 195 200 205
 Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr
 210 215 220
 Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 225 230 235 240
 Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro
 245 250 255
 Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys
 260 265 270
 Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr
 275 280 285
 Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser
 290 295 300
 Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly
 305 310 315 320
 Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala
 325 330 335
 Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly

340

345

350

Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly
 355 360 365

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
 370 375 380

Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
 385 390 395 400

Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly
 405 410 415

Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr
 420 425 430

Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu
 435 440 445

Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp
 450 455 460

Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg
 465 470 475 480

Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
 485 490 495

Ser Ser

<210> 340
 <211> 1497
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH5VL2xCD19 HLLH

<400> 340
 gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg 60
 tcttgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120
 cctggacagg gtctggaatg gattggatac attaataccta gccgtgggta tactaattac 180
 gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240

atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcctcaggc 360
 gaagg tacta gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacattgta 420
 ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480
 agagccagtc aaagtgtgaa ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
 acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaagggtg 720
 gagatcaaat ccggagggtg tggatccgat atccagctga ccagctctcc agcttctttg 780
 gctgtgtctc tagggcagag ggccaccatc tcctgcaagg ccagccaaag tgttgattat 840
 gatggtgata gttatttgaa ctggtaccaa cagattccag gacagccacc caaactctc 900
 atctatgatg catccaatct agtttctggg atcccacca ggttagtggt cagtgggtct 960
 gggacagact tcacctcaa catccatcct gtggagaagg tggatgctgc aacctatcac 1020
 tgtcagcaaa gtactgagga tccgtggacg ttcggtggag ggaccaagct cgagatcaaa 1080
 ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctcaggt gcagctgcag 1140
 cagtctgggg ctgagctggt gaggcctggg tcctcagtga agatttctg caaggcttct 1200
 ggctatgcat tcagtagcta ctggatgaac tgggtgaagc agaggcctgg acagggtctt 1260
 gagtggattg gacagatttg gcctggagat ggtgatacta actacaatgg aaagttcaag 1320
 ggtaaagcca ctctgactgc agacgaatcc tccagcacag cctacatgca actcagcagc 1380
 ctagcatctg aggactctgc ggtctatttc tgtgcaagac gggagactac gacggtaggc 1440
 cgttattact atgctatgga ctactggggc caagggacca cggtcaccgt ctcctcc 1497

<210> 341

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> VH5VL2xCD19 HLLH

<400> 341

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr

20					25					30					
Thr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile
	35						40					45			
Gly	Tyr	Ile	Asn	Pro	Ser	Arg	Gly	Tyr	Thr	Asn	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Thr	Thr	Asp	Lys	Ser	Thr	Ser	Thr	Ala	Tyr
	65					70					75				80
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Thr	Tyr	Tyr	Cys
				85					90					95	
Ala	Arg	Tyr	Tyr	Asp	Asp	His	Tyr	Cys	Leu	Asp	Tyr	Trp	Gly	Gln	Gly
			100					105						110	
Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Glu	Gly	Thr	Ser	Thr	Gly	Ser	Gly
		115					120					125			
Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ala	Asp	Asp	Ile	Val	Leu	Thr	Gln	Ser
	130					135					140				
Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly	Glu	Arg	Ala	Thr	Leu	Ser	Cys
	145					150					155				160
Arg	Ala	Ser	Gln	Ser	Val	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Pro
				165					170					175	
Gly	Lys	Ala	Pro	Lys	Arg	Trp	Ile	Tyr	Asp	Thr	Ser	Lys	Val	Ala	Ser
			180					185					190		
Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Ser
	195						200					205			
Leu	Thr	Ile	Asn	Ser	Leu	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys
	210					215					220				
Gln	Gln	Trp	Ser	Ser	Asn	Pro	Leu	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val
	225					230					235				240
Glu	Ile	Lys	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Gln	Leu	Thr	Gln	Ser
				245					250					255	

Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys
 260 265 270

Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp
 275 280 285

Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala
 290 295 300

Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser
 305 310 315 320

Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala
 325 330 335

Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly
 340 345 350

Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly
 355 360 365

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala
 370 375 380

Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser
 385 390 395 400

Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro
 405 410 415

Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp
 420 425 430

Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp
 435 440 445

Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu
 450 455 460

Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly
 465 470 475 480

Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 485 490 495

Val Ser Ser

<210> 342
 <211> 1494
 <212> DNA
 <213> artificial sequence

<220>
 <223> VL3VH5xCD19 LHHL

<400> 342
 gacattgtac tgacccagtc tccagcaact ctgtctctgt ctccagggga gcgtgccacc 60
 ctgacctgca gagccagttc aagtgttaagt tacatgaact ggtaccagca gaagccgggc 120
 aaggcaccga aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
 ttcagtggca gtgggtctgg gaccgactac tctctcaca tcaacagctt ggaggctgaa 240
 gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cggtggcggg 300
 accaagggtg agatcaaagg cgaaggtagt agtactggtt ctggtggaag tggaggttca 360
 ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
 tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
 gtaaggcagg cacctggaca ggggtctggaa tggattggat acattaatcc tagccgtggt 540
 tatactaatt acgcagacag cgtcaagggc cgcttcacaa tcactacaga caaatccacc 600
 agcacagcct acatggaact gagcagcctg cgttctgagg aactgcaac ctattactgt 660
 gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc 720
 gtctcctccg gaggtggtgg atcccagggtg cagctgcagc agtctggggc tgagctggtg 780
 aggctgggt cctcagtga gatttcctgc aaggcttctg gctatgcatt cagtagctac 840
 tggatgaact gggatgaagca gaggcctgga cagggtcttg agtggattgg acagatttgg 900
 cctggagatg gtgatactaa ctacaatgga aagttcaagg gtaaagccac tctgactgca 960
 gacgaatcct ccagcacagc ctacatgcaa ctacagagcc tagcatctga ggactctgcg 1020
 gtctatttct gtgcaagacg ggagactacg acggtaggac gttattacta tgctatggac 1080
 tactggggcc aagggaccac ggtcacgctc tctccggtg gtggtggttc tggcggcggc 1140
 ggctccggtg gtggtggttc tgatatccag ctgacccagt ctccagcttc tttggctgtg 1200
 tctctagggc agagggccac catctcctgc aaggccagcc aaagtgttga ttatgatggt 1260
 gatagttatt tgaactggta ccaacagatt ccaggacagc caccctaaact cctcatctat 1320
 gatgcatcca atctagtttc tgggatccca cccaggttta gtggcagtggt gtctgggaca 1380

gacttcaccc tcaacatcca tctgtggag aagggtggatg ctgcaaccta tcactgtcag 1440

caaagtactg aggatccgtg gacgttcggt ggagggacca agctcgagat caaa 1494

<210> 343

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> VL3VH5xCD19 LHHL

<400> 343

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe
 180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr
 210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly
 245 250 255

Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala
 260 265 270

Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg
 275 280 285

Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly
 290 295 300

Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala
 305 310 315 320

Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser
 325 330 335

Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val
 340 345 350

Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val
 385 390 395 400

Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val
 405 410 415

Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly
 420 425 430

Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly
 435 440 445

Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 450 455 460

Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln
 465 470 475 480

Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
 485 490 495

Ile Lys

<210> 344
 <211> 1497
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH5VL3xCD19 HLHL

<400> 344
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 cctggacagg gtctggaatg gattggatac attaatccta gccgtgggtta tactaattac 180
 gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 240
 atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
 gaagggtacta gtactgggtc tgggtggaagt ggagggttcag gtggagcaga cgacattgta 420
 ctgaccagct ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgacctgc 480
 agagccagtt caagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcacc 540
 aaaagatgga tttatgacac atccaaagt gcttctggag tccctgctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
 acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaagggtg 720

gagatcaaat ccggaggtgg tggatcccag gtgcagctgc agcagtctgg ggctgagctg 780
 gtgaggcctg ggtcctcagt gaagatttcc tgcaaggctt ctggctatgc attcagtagc 840
 tactggatga actgggtgaa gcagaggcct ggacagggtc ttgagtggat tggacagatt 900
 tggcctggag atggtgatac taactacaat ggaaagtcca agggtaaagc cactctgact 960
 gcagacgaat cctccagcac agcctacatg caactcagca gcctagcatc tgaggactct 1020
 gcggtctatt tctgtgcaag acgggagact acgacggtag gccgttatta ctatgctatg 1080
 gactactggg gccaaaggac cacggtcacc gtctcctccg gtggtgggtg ttctggcggc 1140
 ggcggctccg gtggtgggtg ttctgatatc cagctgacct agtctccagc ttctttggct 1200
 gtgtctctag ggcagagggc caccatctcc tgcaaggcca gccaaagtgt tgattatgat 1260
 ggtgatagtt atttgaactg gtaccaacag attccaggac agccacccaa actcctcatc 1320
 tatgatgcat ccaatctagt ttctgggatc ccaccaggt ttagtggcag tgggtctggg 1380
 acagactica ccctcaacat ccctcctgtg gagaagggtg atgctgcaac ctatcactgt 1440
 cagcaaagta ctgaggatcc gtggacgttc ggtggaggga ccaagctcga gatcaaa 1497

<210> 345

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> VH5VL3xCD19 HLHL

<400> 345

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
 145 150 155 160

Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser
 245 250 255

Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys
 260 265 270

Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln
 275 280 285

Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp
 290 295 300

Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr
 305 310 315 320

Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala

325 330 335
 Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr
 340 345 350
 Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr
 355 360 365
 Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380
 Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala
 385 390 395 400
 Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser
 405 410 415
 Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro
 420 425 430
 Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser
 435 440 445
 Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 450 455 460
 Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys
 465 470 475 480
 Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
 485 490 495
 Glu Ile Lys

<210> 346
 <211> 1494
 <212> DNA
 <213> artificial sequence

<220>
 <223> VL3VH5xCD19 LHLH

<400> 346
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 ctgacctgca gagccagttc aagtgttaagt tacatgaact ggtaccagca gaagccgggc 120

aaggcaccca aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
gatgctgccca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cgggtggcggg 300
accaaggtgg agatcaaagg cgaagggtact agtactgggt ctggtggaag tggaggttca 360
gggtggagcag acgacgtcca actgggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggg 540
tatactaatt acgcagacag cgtcaagggc cgcttcacia tcactacaga caaatccacc 600
agcacagcct acatggaact gagcagcctg cgttctgagg aactgcaac ctattactgt 660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc 720
gtctcctccg gaggtgggtg atccgatata cagctgaccc agtctccagc ttctttgggt 780
gtgtctctag ggcagagggc caccatctcc tgcaaggcca gccaaagtgt tgattatgat 840
ggatgatagtt atttgaactg gtaccaacag attccaggac agccacccaa actcctcatc 900
tatgatgat ccaatctagt ttctgggatc ccaccaggt ttagtggcag tgggtctggg 960
acagacttca ccctcaacat ccatcctgtg gagaaggtgg atgctgcaac ctatcactgt 1020
cagcaaagta ctgaggatcc gtggacgttc ggtggaggga ccaagctcga gatcaaaggt 1080
gggtgggtggt ctggcggcgg cggctccggt ggtgggtggt ctcagggtgca gctgcagcag 1140
tctggggctg agctgggtgag gcctgggtcc tcagtgaaga tttctgcaa ggcttctggc 1200
tatgcattca gtagctactg gatgaactgg gtgaagcaga ggcctggaca gggctctgag 1260
tggattggac agatttggcc tggagatggt gatactaact acaatggaaa gttcaagggt 1320
aaagccactc tgactgcaga cgaatcctcc agcacagcct acatgcaact cagcagccta 1380
gcatctgagg actctgcggt ctatttctgt gcaagacggg agactacgac ggtaggccgt 1440
tattactatg ctatggacta ctggggccaa gggaccaggg tcaccgtctc ctcc 1494

<210> 347

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> VL3VH5xCD19 LHLH

<400> 347

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly

1	5	10	15
Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met	20	25	30
Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr	35	40	45
Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser	50	55	60
Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu	65	70	75
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr	85	90	95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr	100	105	110
Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu	115	120	125
Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val	130	135	140
Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp	145	150	155
Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn	165	170	175
Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe	180	185	190
Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser	195	200	205
Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr	210	215	220
Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr	225	230	235
			240

Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys
260 265 270

Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr
275 280 285

Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser
290 295 300

Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly
305 310 315 320

Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala
325 330 335

Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly
340 345 350

Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly
355 360 365

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
370 375 380

Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
385 390 395 400

Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly
405 410 415

Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr
420 425 430

Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu
435 440 445

Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp
450 455 460

Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg
465 470 475 480

<210>	348
<211>	1497
<212>	DNA
<213>	artificial sequence

<220>
<223> VH5VL3xCD19 HLLH

<400>	348					
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cctggacagg	gtctggaatg	gattggatac	attaatccta	gccgtggtta	tactaattac	180
gcagacagcg	tcaagggccg	cttcacaatc	actacagaca	aatccaccag	cacagcctac	240
atggaactga	gcagcctgcg	ttctgaggac	actgcaacct	attactgtgc	aagatattat	300
gatgatcatt	actgccttga	ctactggggc	caaggcacca	cggtcacctg	ctcctcaggc	360
gaaggtacta	gtactggttc	tggtggaagt	ggaggttcag	gtggagcaga	cgacattgta	420
ctgaccagtc	ctccagcaac	tctgtctctg	tctccagggg	agcgtgccac	cctgacctgc	480
agagccagtt	caagtgtgaag	ttacatgaac	tggtaccagc	agaagccggg	caaggcaccc	540
aaaagatgga	tttatgacac	atccaaagtg	gcttctggag	tccttgctcg	cttcagtggc	600
agtgggtctg	ggaccgacta	ctctctcaca	atcaacagct	tggaggctga	agatgctgcc	660
acttattact	gccaacagtg	gagtagtaac	ccgctcacgt	tcggtggcgg	gaccaaggtg	720
gagatcaaat	ccggagggtg	tggatccgat	atccagctga	cccagtctcc	agcttctttg	780
gctgtgtctc	tagggcagag	ggccaccatc	tcctgcaagg	ccagccaaag	tgttgattat	840
gatggtgata	gttatttgaa	ctggtaccaa	cagattccag	gacagccacc	caaactcctc	900
atctatgatg	catccaatct	agtttctggg	atcccaccca	ggtttagtg	cagtgggtct	960
gggacagact	tcacctctaa	catccatcct	gtggagaagg	tggatgctgc	aacctatcac	1020
tgtcagcaaa	gtactgagga	tccgtggacg	ttcggtggag	ggaccaagct	cgagatcaaa	1080
ggtggtggtg	gttctggcgg	cggcggctcc	ggtggtggtg	gttctcaggt	gcagctgcag	1140
cagtctgggg	ctgagctggt	gaggcctggg	tcctcagtga	agatttcctg	caaggcttct	1200
ggctatgcat	tcagtagcta	ctggatgaac	tgggtgaagc	agaggcctgg	acagggtctt	1260

gagtggattg gacagatttg gcctggagat ggtgatacta actacaatgg aaagttcaag 1320
 ggtaaagcca ctctgactgc agacgaatcc tccagcacag cctacatgca actcagcagc 1380
 ctagcatctg aggactctgc ggtctatttc tgtgcaagac gggagactac gacggtaggc 1440
 cgttattact atgctatgga ctactggggc caagggacca cggtcaccgt ctctctcc 1497

<210> 349
 <211> 499
 <212> PRT
 <213> artificial sequence

<220>
 <223> VH5VL3xCD19 HLLH

<400> 349

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
 145 150 155 160

Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser
 245 250 255

Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys
 260 265 270

Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp
 275 280 285

Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala
 290 295 300

Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser
 305 310 315 320

Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala
 325 330 335

Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly
 340 345 350

Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly
 355 360 365

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala
 370 375 380

Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser
 385 390 395 400

Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro
 405 410 415

Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp
 420 425 430

Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp
 435 440 445

Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu
 450 455 460

Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly
 465 470 475 480

Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 485 490 495

Val Ser Ser

<210> 350

<211> 1494

<212> DNA

<213> artificial sequence

<220>

<223> VL1VH7xCD19 LHHL

<400> 350

gacattcaga tgaccagtc tccatctagc ctgtctgcat ctgtcgggga ccgtgtcacc 60

atcacctgca gagccagtca aagtgtaagt tacatgaact ggtaccagca gaagccgggc 120

aaggcaccga aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctgcg 180

ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240

gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cgggtggcggg 300

accaaggtgg agatcaaagg cgaaggtact agtactgggt ctggtggaag tggaggttca 360

gggtggagcag acgacgtcca actgggtgcag tcaggggctg aagtgaaaaa acctggggcc 420

tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480

gtaaggcagg cacctggaca ggggtctggaa tggattggat acattaatcc tagccgtggt 540

tatactaatt acaatcagaa gttcaaggac cgcgtcacia tctactacaga caaatccacc 600

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agcacagcct acatggaact gagcagcctg cgttctgagg aactgcagt ctattactgt    660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc    720
gtctcctccg gaggtggtgg atcccagggtg cagctgcagc agtctggggc tgagctggtg    780
aggcctgggt cctcagtga gatttcctgc aaggcttctg gctatgcatt cagtagctac    840
tggatgaact gggatgaagca gaggcctgga cagggtcttg agtggattgg acagatttgg    900
cctggagatg gtgatactaa ctacaatgga aagttcaagg gtaaagccac tctgactgca    960
gacgaatcct ccagcacagc ctacatgcaa ctcagcagcc tagcatctga ggactctgcg   1020
gtctatttct gtgcaagacg ggagactacg acggtaggcc gttattacta tgctatggac   1080
tactggggcc aaggggaccac ggtcaccgtc tctcgggtg gtggtggttc tggcggcggc   1140
ggctccgggtg gtggtggttc tgatatccag ctgaccagct ctccagcttc tttggctgtg   1200
tctctagggc agagggccac catctcctgc aaggccagcc aaagtgttga ttatgatggt   1260
gatagttatt tgaactggtg ccaacagatt ccaggacagc caccctaaact cctcatctat   1320
gatgcattca atctagtttc tgggatccca cccagggtta gtggcagtggt gtctgggaca   1380
gacttcaccc tcaacatcca tctgtggag aaggtggatg ctgcaacctc tcaactgtcag   1440
caaagtactg aggatccgtg gacgttcggt ggagggacca agctcgagat caaa         1494

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<210> 351

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> VL1VH7xCD19 LHHL

<400> 351

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1           5           10          15

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
20           25           30

```

```

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35           40           45

```

```

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50           55           60

```

```

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65           70           75           80

```


Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
 100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
 115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
 145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
 180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr
 210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly
 245 250 255

Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala
 260 265 270

Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg
 275 280 285

Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly
 290 295 300

Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala

305 310 315 320
 Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser
 325 330 335
 Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val
 340 345 350
 Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val
 355 360 365
 Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380
 Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val
 385 390 395 400
 Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val
 405 410 415
 Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly
 420 425 430
 Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly
 435 440 445
 Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 450 455 460
 Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln
 465 470 475 480
 Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
 485 490 495

Ile Lys

<210> 352
 <211> 1497
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH7VL1xCD19 HLHL

<400> 352
gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaaggtg 60
tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120
cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 180
aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac 240
atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat 300
gatgatcatt actgcottga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
gaaggtacta gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacattcag 420
atgaccagtc ctccatctag cctgtctgca tctgtcgggg accgtgtcac catcacctgc 480
agagccagtc aaagtgtgaa ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
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acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg 720
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acagacttca cctcaacat ccctcctgtg gagaaggtgg atgctgcaac ctatcactgt 1440
cagcaaagta ctgaggatcc gtggacgttc ggtggaggga ccaagctcga gatcaaa 1497

<210> 353

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> VH7VL1xCD19 HLHL

<400> 353

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
 50 55 60

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser
 130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
 145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser
 245 250 255

Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys
 260 265 270

Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln
 275 280 285

Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp
 290 295 300

Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr
 305 310 315 320

Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala
 325 330 335

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr
 340 345 350

Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr
 355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380

Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala
 385 390 395 400

Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser
 405 410 415

Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro
 420 425 430

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser
 435 440 445

Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 450 455 460

Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys
 465 470 475 480

Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
 485 490 495

Glu Ile Lys

<210> 354
 <211> 1494
 <212> DNA
 <213> artificial sequence

<220>
 <223> VL1VH7xCD19 LHLH

<400> 354
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 aaggcaccca aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
 ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
 gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cgggtggcggg 300
 accaagggtg agatcaaagg cgaagggtact agtactgggt ctggtggaag tggagggttca 360
 ggtggagcag acgacgtcca actgggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
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 gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggt 540
 tatactaatt acaatcagaa gttcaaggac cgcgtcacia tctactacaga caaatccacc 600
 agcacagcct acatggaact gagcagcctg cgcttctgagg aactgcagt ctattactgt 660
 gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc 720
 gtctctctcg gaggtggtgg atccgatatc cagctgaccc agtctccagc ttcttttggt 780
 gtgtctctag ggcagagggc caccatctcc tgcaaggcca gccaaagtgt tgattatgat 840
 ggtgatagtt atttgaactg gtaccaacag attccaggac agccacccaa actcctcatc 900
 tatgatgcat ccaatctagt ttctgggatc ccaccaggt ttagtggcag tgggtctggg 960
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 cagcaaagta ctgaggatcc gtggacgttc ggtggaggga ccaagctcga gatcaaaggt 1080
 ggtggtggtt ctggcggcgg cggtccggt ggtggtggtt ctgaggtgca gctgcagcag 1140

tctggggctg agctggtgag gcctgggtcc tcagtgaaga tttcctgcaa ggcttctggc 1200
 tatgcattca gtagctactg gatgaactgg gtgaagcaga ggcctggaca gggctcttgag 1260
 tggattggac agatttggcc tggagatggt gatactaact acaatggaaa gttcaagggt 1320
 aaagccactc tgactgcaga cgaatcctcc agcacagcct acatgcaact cagcagccta 1380
 gcatctgagg actctgcggt ctatttctgt gcaagacggg agactacgac ggtaggccgt 1440
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<210> 355

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> VL1VH7xCD19 LHLH

<400> 355

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
 20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
 35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
 100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
 115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
 145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
 180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr
 210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro
 245 250 255

Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys
 260 265 270

Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr
 275 280 285

Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser
 290 295 300

Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly
 305 310 315 320

Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala
 325 330 335

Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly
 340 345 350

Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly
 355 360 365

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
 370 375 380

Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
385 390 395 400

Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly
405 410 415

Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr
420 425 430

Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu
435 440 445

Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp
450 455 460

Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg
465 470 475 480

Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
485 490 495

Ser Ser

<210> 356
<211> 1497
<212> DNA
<213> artificial sequence

<220>
<223> VH7VL1xCD19 HLLH

<400> 356
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cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 180
aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac 240
atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat 300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctccctcaggc 360
gaagggtacta gtactgggtc tgggtggaagt ggaggttcag gtggagcaga cgacattcag 420
atgaccagct ctccatctag cctgtctgca tctgtcgggg accgtgtcac catcacctgc 480

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agagccagtc aaagtgtaag ttacatgaac tggtagcagc agaagccggg caaggcaccc 540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg 720
gagatcaaat ccggaggtgg tggatccgat atccagctga cccagtctcc agcttctttg 780
gctgtgtctc tagggcagag ggccaccatc tcctgcaagg ccagccaaag tgttgattat 840
gatggtgata gttatttgaa ctggtaccaa cagattccag gacagccacc caaactctc 900
atctatgatg catccaatct agtttctggg atcccaccca ggtttagtgg cagtgggtct 960
gggacagact tcacctcaa catccatcct gtggagaagg tggatgctgc aacctatcac 1020
tgtcagcaaa gtactgagga tccgtggacg ttcggtggag ggaccaagct cgagatcaaa 1080
ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctcaggt gcagctgcag 1140
cagtctgggg ctgagctggt gaggcctggg tcctcagtga agatttctg caaggcttct 1200
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gagtggattg gacagatttg gcctggagat ggtgatacta actacaatgg aaagttcaag 1320
ggtaaagcca ctctgactgc agacgaatcc tccagcacag cctacatgca actcagcagc 1380
ctagcatctg aggactctgc ggtctatttc tgtgcaagac gggagactac gacggtaggc 1440
cgttattact atgctatgga ctactggggc caagggacca cggtcaccgt ctctctcc 1497

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<210> 357

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> VH7VL1xCD19 HLLH

<400> 357

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Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1           5           10           15

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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20           25           30

```

```

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35           40           45

```

```

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
50           55           60

```

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser
130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser
245 250 255

Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys
260 265 270

Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp
275 280 285

Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala

290

295

300

Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser
 305 310 315 320

Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala
 325 330 335

Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly
 340 345 350

Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly
 355 360 365

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala
 370 375 380

Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser
 385 390 395 400

Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro
 405 410 415

Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp
 420 425 430

Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp
 435 440 445

Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu
 450 455 460

Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly
 465 470 475 480

Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 485 490 495

Val Ser Ser

<210> 358

<211> 1494

<212> DNA

<213> artificial sequence

<220>

<223> VL2VH7xCD19 LHHL

<400> 358

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aaggcaccca aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc	180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa	240
gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cgggtggcggg	300
accaaggtgg agatcaaagg cgaagggtact agtactgggt ctggtggaag tggaggttca	360
ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc	420
tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg	480
gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggt	540
tatactaatt acaatcagaa gttcaaggac cgcgtcacia tcactacaga caaatccacc	600
agcacagcct acatggaact gagcagcctg cgctctgagg aactgcagt ctattactgt	660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc	720
gtctcctccg gaggtggtgg atcccagggt cagctgcagc agtctggggc tgagctggtg	780
aggcctgggt cctcagtga gatttcctgc aaggcttctg gctatgcatt cagtagctac	840
tggatgaact ggggtgaagca gaggcctgga cagggtcttg agtggattgg acagatttgg	900
cctggagatg gtgatactaa ctacaatgga aagttcaagg gtaaagccac tctgactgca	960
gacgaatcct ccagcacagc ctacatgcaa ctacagcagc tagcatctga ggactctgcg	1020
gtctatttct gtgcaagacg ggagactacg acggtaggcc gttattacta tgctatggac	1080
tactggggcc aagggaccac ggtcacctgc tcctccggtg gtggtggttc tggcggcggc	1140
ggctccggtg gtggtggttc tgatatccag ctgaccagc ctccagcttc tttggctgtg	1200
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gatagttatt tgaactggta ccaacagatt ccaggacagc caccctaaact cctcatctat	1320
gatgcatcca atctagtttc tgggatccca ccaggttta gtggcagtgg gtctgggaca	1380
gacttcaccc tcaacatcca tcctgtggag aagggtggat ctgcaaccta tcaactgtcag	1440
caaagtactg aggatccgtg gacgttcggt ggagggacca agctcgagat caaa	1494

<210> 359

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> VL2VH7xCD19 LHHL

<400> 359

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr
 210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly
 245 250 255

Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala
 260 265 270

Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg
 275 280 285

Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly
 290 295 300

Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala
 305 310 315 320

Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser
 325 330 335

Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val
 340 345 350

Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val
 385 390 395 400

Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val
 405 410 415

Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly
 420 425 430

Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly
 435 440 445

Ile Pro Pro Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu
 450 455 460

Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln
 465 470 475 480

Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
 485 490 495

Ile Lys

<210> 360
 <211> 1497
 <212> DNA
 <213> artificial sequence

<220>
 <223> VH7VL2xCD19 HLHL

<400> 360
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 cctggacagg gtctggaatg gattggatac attaatccta gccgtgggtta tactaattac 180
 aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac 240
 atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctccctcaggc 360
 gaagggtacta gtactggttc tgggtggaagt ggaggttcag gtggagcaga cgacattgta 420
 ctgacctcagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480
 agagccagtc aaagtgtgaa ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggagggtga agatgctgcc 660
 acttattact gccaacagtg gagtagtaac ccgctcacgt tcgggtggcgg gaccaagggtg 720
 gagatcaaat ccggagggtg tggatccag gtgcagctgc agcagtctgg ggctgagctg 780
 gtgaggcctg ggtcctcagt gaagatttcc tgcaaggctt ctggctatgc attcagtagc 840
 tactggatga actgggtgaa gcagaggcct ggacagggtc ttgagtggat tggacagatt 900
 tggcctggag atggtgatac taactacaat ggaaagttca agggtaaagc cactctgact 960
 gcagacgaat cctccagcac agcctacatg caactcagca gcctagcatc tgaggactct 1020

gcggtctatt tctgtgcaag acgggagact acgacggtag gccgttatta ctatgctatg 1080
gactactggg gccaaaggac cacggtcacc gtctcctccg gtgggtggtgg ttctggcggc 1140
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gtgtctctag ggcagagggc caccatctcc tgcaaggcca gccaaagtgt tgattatgat 1260
ggtgatagtt atttgaactg gtaccaacag attccaggac agccacccaa actcctcatc 1320
tatgatgcat ccaatctagt ttctgggata ccaccaggt ttagtggcag tgggtctggg 1380
acagacttca ccctcaacat ccctcctgtg gagaagggtg atgctgcaac ctatcactgt 1440
cagcaaagta ctgaggatcc gtggacgttc ggtggaggga ccaagctcga gatcaaa 1497

<210> 361
<211> 499
<212> PRT
<213> artificial sequence

<220>
<223> VH7VL2xCD19 HLHL

<400> 361

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser
 245 250 255

Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys
 260 265 270

Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln
 275 280 285

Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp
 290 295 300

Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr
 305 310 315 320

Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala
 325 330 335

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr
 340 345 350

Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr
 355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala
385 390 395 400

Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser
405 410 415

Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro
420 425 430

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser
435 440 445

Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
450 455 460

Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys
465 470 475 480

Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
485 490 495

Glu Ile Lys

<210> 362
<211> 1494
<212> DNA
<213> artificial sequence

<220>
<223> VL2VH7xCD19 LHLH

<400> 362
gacattgtac tgaccagtc tccagcaact ctgtctctgt ctccagggga gcgtgccacc 60
ctgagctgca gagccagtca aagtgttaagt tacatgaact ggtaccagca gaagccgggc 120
aaggcaccga aaagatggat ttatgacaca tccaaagtgg cttctggagt cctgtctcgc 180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
gatgctgccca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cggtggcggg 300
accaaggtgg agatcaaagg cgaaggtact agtactgggt ctggtggaag tggaggttca 360

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ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctgggggc 420
tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggt 540
tatactaatt acaatcagaa gttcaaggac cgcgtcacia tcaactacaga caaatccacc 600
agcacagcct acatggaact gagcagcctg cgttctgagg aactgcagt ctattactgt 660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc 720
gtctcctccg gaggtggtgg atccgatatc cagctgaccc agtctccagc ttctttggct 780
gtgtctctag ggcagagggc caccatctcc tgcaaggcca gccaaagtgt tgattatgat 840
ggtgatagtt atttgaactg gtaccaacag attccaggac agccacccaa actcctcatc 900
tatgatgcat ccaatctagt ttctgggatc ccaccagggt ttagtggcag tgggtctggg 960
acagacttca ccctcaacat ccctcctgtg gagaagggtg atgctgcaac ctatcactgt 1020
cagcaaagta ctgaggatcc gtggacgttc ggtggaggga ccaagctcga gatcaaagg 1080
ggtggtggtt ctggcggcgg cggtccggt ggtggtggtt ctgaggtgca gctgcagcag 1140
tctggggctg agctggtgag gcctgggtcc tcagtgaaga ttctctgcaa ggcttctggc 1200
tatgcattca gtagctactg gatgaactgg gtgaagcaga ggctggaca gggctctgag 1260
tggattggac agatttggcc tggagatggt gatactaact acaatggaaa gttcaagggt 1320
aaagccactc tgactgcaga cgaatcctcc agcacagcct acatgcaact cagcagccta 1380
gcatctgagg actctgcggt ctatttctgt gcaagacggg agactacgac ggtaggccgt 1440
tattactatg ctatggacta ctggggccaa gggaccacgg tcaccgtctc ctcc 1494

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<210> 363
 <211> 498
 <212> PRT
 <213> artificial sequence

<220>
 <223> VL2VH7xCD19 LHLH

<400> 363

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
 20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
 35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
 100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
 115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
 145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
 180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr
 210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro
 245 250 255

Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys
 260 265 270

Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr

275		280		285
Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser				
290		295		300
Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly				
305		310		315 320
Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala				
		325		330 335
Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly				
		340		345 350
Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly				
		355		360 365
Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu				
		370		375 380
Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly				
		385		390 395 400
Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly				
		405		410 415
Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr				
		420		425 430
Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu				
		435		440 445
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp				
		450		455 460
Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg				
		465		470 475 480
Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val				
		485		490 495
Ser Ser				

<210> 364
<211> 1497
<212> DNA
<213> artificial sequence

<220>
<223> VH7VL2xCD19 HLLH

<400> 364
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cctggacagg gtctggaatg gattggatac attaataccta gccgtgggta tactaattac 180
aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac 240
atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat 300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc 360
gaaggctacta gtactgggtc tggatggaag ggaggttcag gtggagcaga cgacattgta 420
ctgaccagtc ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgagctgc 480
agagccagtc aaagtgtgaa ttacatgaac tggatccagc agaagccggg caaggcaccc 540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcgggtggcg gaccaaggtg 720
gagatcaaat ccggaggtgg tggatccgat atccagctga ccagctctcc agcttctttg 780
gctgtgtctc tagggcagag ggccaccatc tcctgcaagg ccagccaaag tgttgattat 840
gatgggtgata gttatttgaa ctgggtaccaa cagattccag gacagccacc caaactctc 900
atctatgatg catccaatct agtttctggg atcccacca ggttagtggt cagtgggtct 960
gggacagact tcaccctcaa catccatcct gtggagaagg tggatgctgc aacctatcac 1020
tgtcagcaaa gtactgagga tccgtggacg ttcggtggag ggaccaagct cgagatcaaa 1080
gggtgggtgg gttctggcg cgccggctcc ggtgggtggg gttctcaggc gcagctgcag 1140
cagtctgggg ctgagctggg gaggcctggg tcctcagtga agatttctg caaggcttct 1200
ggctatgcat tcagtagcta ctggatgaac tgggtgaagc agaggcctgg acagggtctt 1260
gagtggattg gacagatttg gcctggagat ggtgatacta actacaatgg aaagttcaag 1320
ggtaaagcca ctctgactgc agacgaatcc tccagcacag cctacatgca actcagcagc 1380
ctagcatctg aggactctgc ggtctatttc tgtgcaagac gggagactac gacggtaggc 1440
cgttattact atgctatgga ctactggggc caagggacca cggtcaccgt ctctccc 1497

<210> 365
 <211> 499
 <212> PRT
 <213> artificial sequence

<220>
 <223> VH7VL2xCD19 HLLH

<400> 365

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
 50 55 60

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 145 150 155 160

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser
 245 250 255

Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys
 260 265 270

Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp
 275 280 285

Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala
 290 295 300

Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser
 305 310 315 320

Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala
 325 330 335

Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly
 340 345 350

Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly
 355 360 365

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala
 370 375 380

Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser
 385 390 395 400

Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro
 405 410 415

Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp
 420 425 430

Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp
 435 440 445

Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu
 450 455 460

Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly
 465 470 475 480

Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 485 490 495

Val Ser Ser

<210> 366
 <211> 1494
 <212> DNA
 <213> artificial sequence

<220>
 <223> VL3VH7xCD19 LHHL

<400> 366
 gacattgtac tgaccagtc tccagcaact ctgtctctgt ctccagggga gcgtgccacc 60
 ctgacctgca gagccagttc aagtgttaagt tacatgaact ggtaccagca gaagccgggc 120
 aaggcaccga aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctgcg 180
 ttcagtggca gtgggtctgg gaccgactac tctctcaca tcaacagctt ggaggctgaa 240
 gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cggtggcggg 300
 accaaggtgg agatcaaagg cgaaggtact agtactggtt ctggtggaag tggaggttca 360
 ggtggagcag acgacgtcca actggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
 tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcaactg 480
 gtaaggcagg cacctggaca gggctctggaa tggattggat acattaatcc tagccgtggt 540
 tatactaatt acaatcagaa gttcaaggac cgcgtcaca tctactacaga caaatccacc 600
 agcacagcct acatggaact gagcagcctg cgttctgagg aactgcagt ctattactgt 660
 gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac cacggtcacc 720
 gtctcctccg gaggtggtgg atcccagggtg cagctgcagc agtctggggc tgagctggtg 780
 aggcctgggt cctcagtga gatttcctgc aaggcttctg gctatgcatt cagtagctac 840
 tggatgaact gggatgaagca gaggcctgga cagggtcttg agtggattgg acagatttgg 900

cctggagatg gtgataactaa ctacaatgga aagttcaagg gtaaagccac tctgactgca 960
 gacgaatcct ccagcacagc ctacatgcaa ctcagcagcc tagcatctga ggactctgcg 1020
 gtctatttct gtgcaagacg ggagactacg acggtaggcc gttattacta tgctatggac 1080
 tactggggcc aagggaccac ggtcaccgtc tcctccggtg gtggtggttc tggcggcgcc 1140
 ggctccggtg gtggtggttc tgatatccag ctgaccagct ctcagcttc tttggctgtg 1200
 tctctagggc agagggccac catctcctgc aaggccagcc aaagtgttga ttatgatggt 1260
 gatagttatt tgaactggta ccaacagatt ccaggacagc caccctaaact cctcatctat 1320
 gatgcatcca atctagtttc tgggatccca ccaggttta gtggcagtgg gtctgggaca 1380
 gacttcaccc tcaacatcca tcctgtggag aaggtggatg ctgcaaccta tcaactgtcag 1440
 caaagtactg aggatccgtg gacgttcggt ggagggacca agctcgagat caaa 1494

<210> 367

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> VL3VH7xCD19 LHHL

<400> 367

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
 20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
 35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
 100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
 115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
 145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
 180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr
 210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly
 245 250 255

Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala
 260 265 270

Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg
 275 280 285

Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly
 290 295 300

Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala
 305 310 315 320

Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser
 325 330 335

Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val
 340 345 350

Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val
 385 390 395 400

Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val
 405 410 415

Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly
 420 425 430

Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly
 435 440 445

Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 450 455 460

Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln
 465 470 475 480

Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
 485 490 495

Ile Lys

<210> 368

<211> 1497

<212> DNA

<213> artificial sequence

<220>

<223> VH7VL3xCD19 HLHL

<400> 368

gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg 60

tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 120

cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac 180

aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac 240

atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat 300
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcttcaggc 360
 gaagg tacta gtactgggttc tgggtggaagt ggaggttcag gtggagcaga cgacattgta 420
 ctgacccagt ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgacctgc 480
 agagccagtt caagtgtgaa ttacatgaac tgggtaccagc agaagccggg caaggcaccc 540
 aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc 600
 agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc 660
 acttattact gccaacagtg gagtagtaac ccgctcacgt tcgggtggcgg gaccaagggtg 720
 gagatcaaat ccggagggtg tggatcccag gtgcagctgc agcagtctgg ggctgagctg 780
 gtgaggcctg ggtcctcagt gaagatttcc tgcaaggctt ctggctatgc attcagtagc 840
 tactggatga actgggtgaa gcagaggcct ggacagggtc ttgagtggat tggacagatt 900
 tggcctggag atggtgatac taactacaat ggaaagtcca agggtaaagc cactctgact 960
 gcagacgaat cctccagcac agcctacatg caactcagca gcctagcatc tgaggactct 1020
 gcggctctatt tctgtgcaag acgggagact acgacggtag gccgttatta ctatgctatg 1080
 gactactggg gccaaaggac cacggtcacc gtctcctccg gtgggtgggtg ttctggcggc 1140
 ggcggtccg gtgggtgggtg ttctgatatc cagctgaccc agtctccagc ttctttggct 1200
 gtgtctctag ggcagagggc caccatctcc tgcaaggcca gccaaagtgt tgattatgat 1260
 ggtgatagtt atttgaactg gtaccaacag attccaggac agccacccaa actcctcatc 1320
 tatgatgcat ccaatctagt ttctgggatc ccaccaggt ttagtggcag tgggtctggg 1380
 acagacttca ccctcaacat ccacctgtg gagaagggtg atgctgcaac ctatcactgt 1440
 cagcaaagta ctgaggatcc gtggacgttc ggtggaggga ccaagctoga gatcaaa 1497

<210> 369

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> VH7VL3xCD19 HLHL

<400> 369

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
 50 55 60
 Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125
 Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140
 Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
 145 150 155 160
 Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175
 Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190
 Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205
 Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220
 Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240
 Glu Ile Lys Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser
 245 250 255
 Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys

260

265

270

Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln
 275 280 285

Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp
 290 295 300

Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr
 305 310 315 320

Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala
 325 330 335

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr
 340 345 350

Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr
 355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380

Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala
 385 390 395 400

Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser
 405 410 415

Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro
 420 425 430

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser
 435 440 445

Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 450 455 460

Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys
 465 470 475 480

Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
 485 490 495

Glu Ile Lys

<210> 370
<211> 1494
<212> DNA
<213> artificial sequence

<220>
<223> VL3VH7xCD19 LHLH

<400> 370
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aaggcaccca aaagatggat ttatgacaca tccaaagtgg cttctggagt ccctgctcgc 180
ttcagtggca gtgggtctgg gaccgactac tctctcacia tcaacagctt ggaggctgaa 240
gatgctgcca cttattactg ccaacagtgg agtagtaacc cgctcacgtt cggtggcggg 300
accaagggtg agatcaaagg cgaaggtagt agtactgggt ctggtggaag tggaggttca 360
gggtggagcag acgacgtcca actgggtgcag tcaggggctg aagtgaaaaa acctggggcc 420
tcagtgaagg tgtcctgcaa ggcttctggc tacaccttta ctaggtacac gatgcactgg 480
gtaaggcagg cacctggaca gggctctgga tggattggat acattaatcc tagccgtggt 540
tatactaatt acaatcagaa gttcaaggac cgcgtcacia tctactacaga caaatccacc 600
agcacagcct acatggaact gagcagcctg cggtctgagg aactgcagt ctattactgt 660
gcaagatatt atgatgatca ttactgcctt gactactggg gccaaaggcac caccgtcacc 720
gtctcctccg gaggtggtgg atccgatatc cagctgaccc agtctccagc ttctttgggt 780
gtgtctctag ggcagagggc caccatctcc tgcaaggcca gccaaagtgt tgattatgat 840
ggatgatagt atttgaactg gtaccaacag attccaggac agccacccaa actcctcatc 900
tatgatgat ccaatctagt ttctgggatc ccaccaggt ttagtggcag tgggtctggg 960
acagacttca ccctcaacat ccatcctgtg gagaagggtg atgctgcaac ctatcactgt 1020
cagcaaagta ctgaggatcc gtggacgttc ggtggaggga ccaagctcga gatcaaagg 1080
gggtggtggt ctggcggcgg cggtccggt ggtggtggt ctcagggtgca gctgcagcag 1140
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tatgattca gtagctactg gatgaactgg gtgaagcaga ggctggaca gggctctgag 1260
tggattggac agatttggcc tggagatggt gatactaact acaatggaaa gttcaagggt 1320
aaagccactc tgactgcaga cgaatcctcc agcacagcct acatgcaact cagcagccta 1380

gcatctgagg actctgcggt ctatttctgt gcaagacggg agactacgac ggtaggccgt 1440

tattactatg ctatggacta ctggggccaa gggaccacgg tcaccgtctc ctcc 1494

<210> 371

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> VL3VH7xCD19 LHLH

<400> 371

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
100 105 110

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
115 120 125

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
130 135 140

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
145 150 155 160

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
165 170 175

Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
 180 185 190

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 195 200 205

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr
 210 215 220

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 225 230 235 240

Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro
 245 250 255

Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys
 260 265 270

Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr
 275 280 285

Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser
 290 295 300

Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly
 305 310 315 320

Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala
 325 330 335

Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly
 340 345 350

Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly
 355 360 365

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
 370 375 380

Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
 385 390 395 400

Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly
 405 410 415

Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr
 420 425 430

Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu
 435 440 445

Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp
 450 455 460

Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg
 465 470 475 480

Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
 485 490 495

Ser Ser

<210> 372

<211> 1497

<212> DNA

<213> artificial sequence

<220>

<223> VH7VL3xCD19 HLLH

<400> 372

gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaaggtg	60
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cctggacagg gtctggaatg gattggatac attaataccta gccgtgggta tactaattac	180
aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac	240
atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat	300
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctcaggc	360
gaaggtacta gtactggttc tgggtggaagt ggagggttcag gtggagcaga cgacattgta	420
ctgaccagtc ctccagcaac tctgtctctg tctccagggg agcgtgccac cctgacctgc	480
agagccagtt caagtgtaag ttacatgaac tgggtaccagc agaagccggg caaggcacc	540
aaaagatgga tttatgacac atccaaagtg gcttctggag tccctgctcg cttcagtggc	600
agtgggtctg ggaccgacta ctctctcaca atcaacagct tggaggctga agatgctgcc	660
acttattact gccaacagtg gagtagtaac ccgctcacgt tcggtggcgg gaccaaggtg	720
gagatcaaat ccggaggtgg tggatccgat atccagctga cccagtctcc agcttctttg	780

gctgtgtctc tagggcagag ggccaccatc tcctgcaagg ccagccaaag tgttgattat 840
 gatggtgata gttatttgaa ctggtaccaa cagattccag gacagccacc caaactcctc 900
 atctatgatg catccaatct agtttctggg atcccaccca ggtttagtgg cagtgggtct 960
 gggacagact tcaccctcaa catccatcct gtggagaagg tggatgctgc aacctatcac 1020
 tgtcagcaaa gtactgagga tccgtggacg ttcggtggag ggaccaagct cgagatcaaa 1080
 ggtggtggtg gttctggcgg cggcggtccc ggtggtggtg gttctcaggt gcagctgcag 1140
 cagtctgggg ctgagctggt gaggcctggg tcctcagtga agatttcctg caaggcttct 1200
 ggctatgcat tcagtagcta ctggatgaac tgggtgaagc agaggcctgg acagggtctt 1260
 gagtggattg gacagatttg gcctggagat ggtgatacta actacaatgg aaagttcaag 1320
 ggtaaagcca ctctgactgc agacgaatcc tccagcacag cctacatgca actcagcagc 1380
 ctagcatctg aggactctgc ggtctatttc tgtgcaagac gggagactac gacggtaggc 1440
 cgttattact atgctatgga ctactggggc caagggacca cggtcacctg ctctctcc 1497

<210> 373

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> VH7VL3xCD19 HLLH

<400> 373

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
 50 55 60

Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 115 120 125

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
 145 150 155 160

Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 195 200 205

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser
 245 250 255

Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys
 260 265 270

Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp
 275 280 285

Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala
 290 295 300

Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser
 305 310 315 320

Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala
 325 330 335

Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly
 340 345 350

Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly
 355 360 365

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala
 370 375 380

Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser
 385 390 395 400

Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro
 405 410 415

Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp
 420 425 430

Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp
 435 440 445

Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu
 450 455 460

Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly
 465 470 475 480

Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 485 490 495

Val Ser Ser

<210> 374

<211> 1497

<212> DNA

<213> artificial sequence

<220>

<223> CD19xVH5/VL1 HLHL

<400> 374

caggtgcagc tgcagcagtc tggggctgag ctggtgaggc ctgggtcctc agtgaagatt 60

tcctgcaagg cttctggcta tgcattcagt agctactgga tgaactgggt gaagcagagg 120

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cctggacagg gtcttgagtg gattggacag atttggcctg gagatggtga tactaactac 180
aatggaaagt tcaagggtaa agccactctg actgcagacg aatcctccag cacagcctac 240
atgcaactca gcagcctagc atctgaggac tctgcggtct atttctgtgc aagacgggag 300
actacgacgg taggccgtta ttactatgct atggactact ggggccaaagg gaccacggtc 360
accgtctcct ccggtggtgg tggttctggc ggcggcggct ccggtggtgg tggttctgat 420
atccagctga cccagtctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc 480
tcctgcaagg ccagccaaag tgttgattat gatggtgata gttatttgaa ctggtaccaa 540
cagattccag gacagccacc caaactcttc atctatgatg catccaatct agtttctggg 600
atcccaccca ggttttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct 660
gtggagaagg tggatgctgc aacctatcac tgtcagcaaa gtactgagga tccgtggacg 720
ttcgggtggag ggaccaagct cgagatcaaa tccggaggtg gtggatccga cgtccaactg 780
gtgcagtcag gggctgaagt gaaaaaacct ggggcctcag tgaagggtgc ctgcaaggct 840
tctggctaca cctttactag gtacacgatg cactgggtaa ggcaggcacc tggacagggg 900
ctggaatgga ttggatacat taatcctagc cgtgggtata ctaattacgc agacagcgtc 960
aagggccgct tcacaatcac tacagacaaa tccaccagca cagcctacat ggaactgagc 1020
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tgccttgact actggggcca aggcaccacg gtcaccgtct cctcaggcga aggtactagt 1140
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ccatctagcc tgtctgcac tgctggggac cgtgtcacca tcacctgcag agccagtcaa 1260
agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcacccaa aagatggatt 1320
tatgacacat ccaaagtggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg 1380
accgactact ctctcacaat caacagcttg gaggtgaag atgctgccac ttattactgc 1440
caacagtgga gtagtaaccc gctcacgttc ggtggcggga ccaaggtgga gatcaaa 1497

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<210> 375

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> CD19xVH5VL1 HLHL

<400> 375

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
130 135 140

Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
145 150 155 160

Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu
165 170 175

Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
180 185 190

Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser
195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val
210 215 220

Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr
225 230 235 240

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser

245	250	255
Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala		
260	265	270
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr		
275	280	285
Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile		
290	295	300
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val		
305	310	315
Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr		
325	330	335
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys		
340	345	350
Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly		
355	360	365
Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly		
370	375	380
Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser		
385	390	395
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys		
405	410	415
Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro		
420	425	430
Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser		
435	440	445
Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser		
450	455	460
Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys		
465	470	475
		480

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 485 490 495

Glu Ile Lys

<210> 376
 <211> 1494
 <212> DNA
 <213> artificial sequence

<220>
 <223> CD19xVL1VH5 LHLH

<400> 376
 gatatccagc tgacccagtc tccagcttct ttggctgtgt ctctagggca gagggccacc 60
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 caacagattc caggacagcc acccaaactc ctcatctatg atgcatcaa tctagtttct 180
 gggatcccac ccaggtttag tggcagtggtg tctgggacag acttcaccct caacatccat 240
 cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg 300
 acgttcggtg gagggaccaa gctcgagatc aaaggtgggtg gtggttctgg cggcggcggc 360
 tccggtggtg gtggttctca ggtgcagctg cagcagtctg gggctgagct ggtgaggcct 420
 gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg 480
 aactgggtga agcagaggcc tggacagggt cttgagtggga ttggacagat ttggcctgga 540
 gatggtgata ctaactacaa tggaaagtgc aagggttaaag ccactctgac tgcagacgaa 600
 tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat 660
 ttctgtgcaa gacgggagac tacgacggta ggccgttatt actatgctat ggactactgg 720
 ggccaaggga ccacgggtcac cgtctcctcc ggaggtgggtg gatccgacat tcagatgacc 780
 cagtctccat ctagcctgtc tgcactctgtc ggggaccgtg tcaccatcac ctgcagagcc 840
 agtcaaagtg taagttacat gaactgggtac cagcagaagc cgggcaaggc acccaaaaga 900
 tggatttatg acacatccaa agtggcttct ggagtcctctg ctgcttcag tggcagtggtg 960
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 tactgccaac agtggagtag taaccgcgtc acgttcggtg gcgggaccaa ggtggagatc 1080
 aaaggcgaag gtactagtag tgggttctggt ggaagtggag gttcaggtgg agcagacgac 1140
 gtccaactgg tgcagtcagg ggctgaagtg aaaaaacctg gggcctcagt gaaggtgtcc 1200
 tgcaaggctt ctggctacac ctttactagg tacacgatgc actgggtaag gcaggcacct 1260

ggacaggggtc tggaatggat tggatacatt aatcctagcc gtgggttatac taattacgca 1320
 gagagcgtca agggccgctt cacaatcact acagacaaat ccaccagcac agcctacatg 1380
 gaactgagca gcctgcgttc tgaggacact gcaacctatt actgtgcaag atattatgat. 1440
 gatcattact gccttgacta ctggggccaa ggcaccacgg tcaccgtctc ctca 1494

<210> 377

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> CD19xVL1VH5 LHLH

<400> 377

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
 20 25 30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
 35 40 45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
 85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
 115 120 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
 130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
 145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
 165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
 180 185 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
 195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
 210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
 225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
 245 250 255

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
 260 265 270

Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn
 275 280 285

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp
 290 295 300

Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly
 305 310 315 320

Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp
 325 330 335

Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe
 340 345 350

Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly
 355 360 365

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val
 370 375 380

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
 385 390 395 400

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val
 405 410 415

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro
 420 425 430

Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr
 435 440 445

Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser
 450 455 460

Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp
 465 470 475 480

Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
 485 490 495

Ser Ser

<210> 378
 <211> 1497
 <212> DNA
 <213> artificial sequence

<220>
 <223> CD19xVL1VH5 HLLH

<400> 378
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 tcctgcaagg cttctggcta tgcattcagt agctactgga tgaactgggt gaagcagagg 120
 cctggacagg gtcttgagtg gattggacag atttggcctg gagatgggtga tactaactac 180
 aatggaaagt tcaagggtaa agccactctg actgcagacg aatcctccag cacagcctac 240
 atgcaactca gcagcctagc atctgaggac tctgcggtct atttctgtgc aagacgggag 300
 actacgacgg taggccgtta ttactatgct atggactact ggggccaagg gaccacggtc 360
 accgtctcct ccggtggtgg tggttctggc ggcggcggct ccggtggtgg tggttctgat 420
 atccagctga ccagctctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc 480
 tcctgcaagg ccagccaaag tgttgattat gatggtgata gttatttgaa ctggtaccaa 540
 cagattccag gacagccacc caaactcctc atctatgatg catccaatct agtttctggg 600
 atcccaccca ggttttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct 660

gtggagaagg tggatgctgc aacctatcac tgtcagcaaa gtactgagga tccgtggacg 720
 ttcggtggag ggaccaagct cgagatcaaa tccggagggtg gtggatccga cattcagatg 780
 acccagtctc catctagcct gtctgcatct gtcggggacc gtgtcaccat cacctgcaga 840
 gccagtcaaa gtgtaagtta catgaactgg taccagcaga agccgggcaa ggcacccaaa 900
 agatggattt atgacacatc caaagtggct tctggagtcc ctgctcgctt cagtggcagt 960
 gggctctggga ccgactactc tctcacaatc aacagcttgg aggctgaaga tgctgccact 1020
 tattactgcc aacagtggag tagtaacccg ctcacgttcg gtggcgggac caaggtggag 1080
 atcaaaggcg aaggtactag tactggttct ggtggaagtg gaggttcagg tggagcagac 1140
 gacgtccaac tggatgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaaggtg 1200
 tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 1260
 cctggacagg gtctggaatg gattggatac attaataccta gccgtgggta tactaattac 1320
 gcagacagcg tcaagggcgc cttcacaatc actacagaca aatccaccag cacagcctac 1380
 atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 1440
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctca 1497

<210> 379

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> CD19xVL1VH5 HLLH

<400> 379

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
 1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
 20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
 65 70 75 80

Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95

Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
 100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
 115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
 130 135 140

Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
 145 150 155 160

Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu
 165 170 175

Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
 180 185 190

Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser
 195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val
 210 215 220

Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr
 225 230 235 240

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser
 245 250 255

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 260 265 270

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
 275 280 285

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
 290 295 300

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 305 310 315 320

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
 325 330 335

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
 340 345 350

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
 355 360 365

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
 370 375 380

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 385 390 395 400

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
 405 410 415

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 420 425 430

Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe
 435 440 445

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 450 455 460

Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr
 465 470 475 480

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 485 490 495

Val Ser Ser

<210> 380

<211> 1497

<212> DNA

<213> artificial sequence

<220>

<223> CD19xVH5VL2 HLHL

<400> 380

cagggtgcagc tgcagcagtc tggggctgag ctgggtgaggc ctgggtcctc agtgaagatt 60
tcctgcaagg cttctggcta tgcattcagt agctactgga tgaactgggt gaagcagagg 120
cctggacagg gtcttgagtg gattggacag atttggcctg gagatgggtga tactaactac 180
aatggaaagt tcaagggtaa agccactctg actgcagacg aatcctccag cacagcctac 240
atgcaactca gcagcctagc atctgaggac tctgcgggtct atttctgtgc aagacgggag 300
actacgacgg taggccgtta ttactatgct atggactact ggggccaaagg gaccacggtc 360
accgtctcct ccggtggtgg tggttctggc ggcggcggct ccggtggtgg tggttctgat 420
atccagctga ccaggtctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc 480
tcctgcaagg ccagccaaag tggtgattat gatggtgata gttatttgaa ctggtaccaa 540
cagattccag gacagccacc caaactcctc atctatgatg catccaatct agtttctggg 600
atccccacca ggtttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct 660
gtggagaagg tggatgctgc aacctatcac tgtcagcaaa gtactgagga tccgtggacg 720
ttcgggtggag ggaccaagct cgagatcaaa tccggagggtg gtggatccga cgtccaactg 780
gtgcagtcag gggctgaagt gaaaaaacct ggggcctcag tgaagggtgc ctgcaaggct 840
tctggctaca cttttactag gtacacgatg cactgggtaa ggcaggcacc tggacagggt 900
ctggaatgga ttggatacat taatcctagc cgtgggtata ctaattacgc agacagcgtc 960
aagggcogct tcacaatcac tacagacaaa tccaccagca cagcctacat ggaactgagc 1020
agcctgogtt ctgaggacac tgcaacctat tactgtgcaa gatattatga tgatcattac 1080
tgccttgact actggggcca aggcaccacg gtcaccgtct cctcaggoga aggtactagt 1140
actggttctg gtggaagtgg aggttcaggt ggagcagacg acattgtact gaccagtcct 1200
ccagcaactc tgtctctgtc tccaggggag cgtgccaccc tgagctgcag agccagtcaa 1260
agtgtgaagt acatgaactg gtaccagcag aagccgggca aggcacccaa aagatggatt 1320
tatgacacat ccaaagtggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg 1380
accgactact ctctcacaat caacagcttg gaggctgaag atgctgccac ttattactgc 1440
caacagtgga gtagtaaccc gctcacgttc ggtggcggga ccaaggtgga gatcaaa 1497

<210> 381

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> CD19xVH5VL2 HLHL

<400> 381

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
 1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
 20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
 65 70 75 80

Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95

Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
 100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
 115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
 130 135 140

Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
 145 150 155 160

Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu
 165 170 175

Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
 180 185 190

Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser
 195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val
 210 215 220

Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr

225		230		235		240
Phe Gly Gly Gly Thr	Lys Leu Glu Ile	Lys Ser Gly Gly Gly Gly Ser				
	245	250			255	
Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala						
	260	265			270	
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr						
	275	280			285	
Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile						
	290	295		300		
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val						
	305	310		315		320
Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr						
	325		330			335
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys						
	340		345			350
Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly						
	355		360			365
Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly						
	370		375		380	
Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser						
	385		390		395	400
Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys						
	405		410			415
Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro						
	420		425			430
Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser						
	435		440		445	
Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser						
	450		455		460	

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 465 470 475 480

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 485 490 495

Glu Ile Lys

<210> 382
 <211> 1494
 <212> DNA
 <213> artificial sequence

<220>
 <223> CD19xVL2VH5 LHLH

<400> 382
 gatatccagc tgaccagtc tccagcttct ttggctgtgt ctctagggca gagggccacc 60
 atctcctgca aggccagcca aagtgttgat tatgatggtg atagttattt gaactggtac 120
 caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 180
 gggatcccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 240
 cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg 300
 acgttcggtg gagggaccaa gctcgagatc aaaggtggtg gtggttcttg cggcggcggc 360
 tccggtggtg gtggttctca ggtgcagctg cagcagctctg gggctgagct ggtgaggcct 420
 gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg 480
 aactgggtga agcagaggcc tggacagggt cttgagtgga ttggacagat ttggcctgga 540
 gatggtgata ctaactacaa tggaaagttc aagggtaaag cactctgac tgcagacgaa 600
 tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat 660
 ttctgtgcaa gacgggagac tacgacggtg ggccgttatt actatgctat ggactactgg 720
 ggccaaggga ccacggtcac cgtctcctcc ggaggtggtg gatccgacat tgtactgacc 780
 cagtctccag caactctgtc tctgtctcca ggggagcgtg ccaccctgag ctgcagagcc 840
 agtcaaagtg taagttacat gaactggtac cagcagaagc cgggcaaggc acccaaaaga 900
 tggatttatg acacatccaa agtggcttct ggagtccttg ctgcttcag tggcagtggg 960
 tctgggaccg actactctct cacaatcaac agcttggagg ctgaagatgc tgccacttat 1020
 tactgccaac agtggagtag taaccgcgtc acgttcggtg gcgggaccaa ggtggagatc 1080
 aaaggcgaag gtactagtag tggttctggt ggaagtggag gttcaggtgg agcagacgac 1140

gtccaactgg tgcagtcagg ggctgaagtg aaaaaacctg gggcctcagt gaaggtgtcc 1200
tgcaaggctt ctggctacac ctttactagg tacacgatgc actgggtaag gcaggcacct 1260
ggacaggggtc tggaatggat tggatacatt aatcctagcc gtggttatac taattacgca 1320
gacagcgtca agggccgctt cacaatcact acagacaaat ccaccagcac agcctacatg 1380
gaactgagca gcctgcgttc tgaggacact gcaacctatt actgtgcaag atattatgat 1440
gatcattact gccttgacta ctgggggcaa ggcaccacgg tcaccgtctc ctca 1494

<210> 383

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> CD19xVL2VH5 LHLH

<400> 383

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
115 120 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
 145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
 165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
 180 185 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
 195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
 210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
 225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
 245 250 255

Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu
 260 265 270

Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn
 275 280 285

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp
 290 295 300

Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly
 305 310 315 320

Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp
 325 330 335

Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe
 340 345 350

Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly
 355 360 365

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val
 370 375 380

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
 385 390 395 400

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val
 405 410 415

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro
 420 425 430

Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr
 435 440 445

Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser
 450 455 460

Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp
 465 470 475 480

Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
 485 490 495

Ser Ser

<210> 384
 <211> 1497
 <212> DNA
 <213> artificial sequence

<220>
 <223> CD19xVL2VH5 HLLH

<400> 384
 caggtgcagc tgcagcagtc tggggctgag ctggtgaggc ctgggtcctc agtgaagatt 60
 tcctgcaagg cttctggcta tgcattcagt agctactgga tgaactgggt gaagcagagg 120
 cctggacagg gtcttgagtg gattggacag atttggcctg gagatggtga tactaactac 180
 aatggaaagt tcaagggtaa agccactctg actgcagacg aatcctccag cacagcctac 240
 atgcaactca gcagcctagc atctgaggac tctgcggtct atttctgtgc aagacgggag 300
 actacgacgg taggccgtta ttactatgct atggactact ggggcccaagg gaccacggtc 360
 accgtctcct ccggtggtgg tggttctggc ggcggcggct ccggtggtgg tggttctgat 420
 atccagctga ccagctctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc 480
 tcctgcaagg ccagccaaag tgttgattat gatggtgata gttatttgaa ctggtaccaa 540

cagattccag gacagccacc caaactcctc atctatgatg catccaatct agtttctggg 600
 atcccaccca ggttttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct 660
 gtggagaagg tggatgctgc aacctatcac tgtcagcaaa gtactgagga tccgtggacg 720
 ttcgggtggag ggaccaagct cgagatcaaa tccggagggtg gtggatccga cattgtactg 780
 acccagtctc cagcaactct gtctctgtct ccaggggagc gtgccaccct gagctgcaga 840
 gccagtcaaa gtgtaagtta catgaactgg taccagcaga agccgggcaa ggcacccaaa 900
 agatggattt atgacaatc caaagtggct tctggagtc ctgctcgctt cagtggcagt 960
 ggggtctggga ccgactactc tctcacaatc aacagcttg aggctgaaga tgctgccact 1020
 tattactgcc aacagtggag tagtaaccgc ctcacgttcg gtggcgggac caaggtggag 1080
 atcaaaggcg aaggtactag tactgggtct ggtggaagtg gaggttcagg tggagcagac 1140
 gacgtccaac tggatgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaaggtg 1200
 tcctgcaagg cttctggcta cacctttact aggtacacga tgactgggt aaggcaggca 1260
 cctggacagg gtctggaatg gattggatac attaactcta gccgtgggta tactaattac 1320
 gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 1380
 atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 1440
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcacctg ctctca 1497

<210> 385
 <211> 499
 <212> PRT
 <213> artificial sequence

<220>
 <223> CD19xVL2VH5 HLLH

<400> 385

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
 1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
 20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
130 135 140

Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
145 150 155 160

Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu
165 170 175

Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
180 185 190

Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser
195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val
210 215 220

Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr
225 230 235 240

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
260 265 270

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
275 280 285

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
290 295 300

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 305 310 315 320

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
 325 330 335

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
 340 345 350

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
 355 360 365

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
 370 375 380

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 385 390 395 400

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
 405 410 415

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 420 425 430

Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe
 435 440 445

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 450 455 460

Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr
 465 470 475 480

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 485 490 495

Val Ser Ser

<210> 386

<211> 1497

<212> DNA

<213> artificial sequence

<220>

<223> CD19xVH5VL3 HLHL

<400> 386

caggtgcagc tgcagcagtc tggggctgag ctggtgaggc ctgggtcctc agtgaagatt	60
tcctgcaagg cttctggcta tgcattcagt agctactgga tgaactgggt gaagcagagg	120
cctggacagg gtcttgagtg gattggacag atttggcctg gagatgggtga tactaactac	180
aatggaaagt tcaagggtaa agccactctg actgcagacg aatcctccag cacagcctac	240
atgcaactca gcagcctagc atctgaggac tctgcggtct atttctgtgc aagacgggag	300
actacgacgg tagggcgtta ttactatgct atggactact ggggccaagg gaccacggtc	360
accgtctcct ccggtggtgg tggttctggc ggcggcggct ccggtggtgg tggttctgat	420
atccagctga cccagtctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc	480
tcctgcaagg ccagccaaag tgttgattat gatggtgata gttatttgaa ctggtaccaa	540
cagattccag gacagccacc caaactcctc atctatgatg catccaatct agtttctggg	600
atcccaccca ggtttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct	660
gtggagaagg tggatgctgc aacctatcac tgtcagcaaa gtactgagga tccgtggacg	720
ttcgggtggag ggaccaagct cgagatcaaa tccggagggtg gtggatccga cgtccaactg	780
gtgcagtcag gggctgaagt gaaaaaacct ggggcctcag tgaagggtgc ctgcaaggct	840
tctggctaca cctttactag gtacacgatg cactgggtaa ggcaggcacc tggacagggt	900
ctggaatgga ttggatacat taatcctagc cgtgggtata ctaattacgc agacagcgtc	960
aagggccgct tcacaatcac tacagacaaa tccaccagca cagcctacat ggaactgagc	1020
agcctgcgtt ctgaggacac tgcaacctat tactgtgcaa gatattatga tgatcattac	1080
tgccttgact actggggcca aggcaccacg gtcaccgtct cctcaggcga aggtactagt	1140
actggttctg gtggaagtgg aggttcaggt ggagcagacg acattgtact gaccagtcct	1200
ccagcaactc tgtctctgtc tccaggggag cgtgccaccc tgacctgcag agccagttca	1260
agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcacccaa aagatggatt	1320
tatgacacat ccaaagtggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg	1380
accgactact ctctcacaat caacagcttg gaggctgaag atgctgccac ttattactgc	1440
caacagtgga gtagtaaccc gctcacgttc ggtggcggga ccaaggtgga gatcaaa	1497

<210> 387

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> CD19xVH5VL3 HLHL

<400> 387

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
130 135 140

Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
145 150 155 160

Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu
165 170 175

Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
180 185 190

Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser
195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val

210

215

220

Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr
 225 230 235 240

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser
 245 250 255

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 260 265 270

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 275 280 285

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 290 295 300

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
 305 310 315 320

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
 325 330 335

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
 340 345 350

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 355 360 365

Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly
 370 375 380

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
 385 390 395 400

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
 405 410 415

Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 420 425 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 435 440 445

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Thr Asp Tyr Ser
 450 455 460

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 465 470 475 480

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 485 490 495

Glu Ile Lys

<210> 388
 <211> 1494
 <212> DNA
 <213> artificial sequence

<220>
 <223> CD19xVL3VH5 LHLH

<400> 388
 gatatccagc tgacccagtc tccagcttct ttggtgtgt ctctagggca gagggccacc 60
 atctcctgca aggccagcca aagtgttgat tatgatggtg atagttattt gaactggtac 120
 caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 180
 gggatcccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 240
 cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg 300
 acgttcggtg gagggaccaa gctcgagatc aaagggtggtg gtggttcttg cggcggcggc 360
 tccggtggtg gtggttctca ggtgcagctg cagcagttctg gggctgagct ggtgaggcct 420
 gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg 480
 aactgggtga agcagaggcc tggacagggt cttgagtga ttggacagat ttggcctgga 540
 gatggtgata ctaactacaa tggaaagttc aagggtaaag ccactctgac tgcagacgaa 600
 tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat 660
 ttctgtgcaa gacgggagac tacgacggta ggccgttatt actatgctat ggactactgg 720
 ggccaaggga ccacggtcac cgtctcctcc ggaggtggtg gatccgacat tgtactgacc 780
 cagtctccag caactctgtc tctgtctcca ggggagcgtg ccaccctgac ctgcagagcc 840
 agttcaagtg taagttacat gaactggtac cagcagaagc cgggcaaggc acccaaaaga 900
 tggatttatg acacatccaa agtggcttct ggagtccctg ctgccttcag tggcagtggg 960
 tctgggaccg actactctct cacaatcaac agcttggagg ctgaagatgc tgccacttat 1020

tactgccaac agtggagtag taacccgctc acgttcggtg gcgggaccaa ggtggagatc 1080
 aaaggcgaag gtactagtac tggttctggt ggaagtggag gttcaggtgg agcagacgac 1140
 gtccaactgg tgcagtcagg ggctgaagtg aaaaaacctg gggcttcagt gaaggtgtcc 1200
 tgcaaggctt ctggctacac ctttactagg tacacgatgc actgggtaag gcaggcacct 1260
 ggacagggtc tggaatggat tggatacatt aatcctagcc gtggttatac taattacgca 1320
 gacagcgtca agggcgcgtt cacaatcact acagacaaat ccaccagcac agcctacatg 1380
 gaactgagca gcctgcgttc tgaggacact gcaacctatt actgtgcaag atattatgat 1440
 gatcattact gccttgacta ctggggccaa ggcaccacgg tcaccgtctc ctca 1494

<210> 389

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> CD19xVL3VH5 LHLH

<400> 389

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
 20 25 30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
 35 40 45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
 85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
 115 120 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
 130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
 145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
 165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
 180 185 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
 195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
 210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
 225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
 245 250 255

Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu
 260 265 270

Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met Asn
 275 280 285

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp
 290 295 300

Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly
 305 310 315 320

Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp
 325 330 335

Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe
 340 345 350

Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly
 355 360 365

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val
370 375 380

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
385 390 395 400

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val
405 410 415

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro
420 425 430

Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr
435 440 445

Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser
450 455 460

Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr Asp
465 470 475 480

Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
485 490 495

Ser Ser

<210> 390

<211> 1497

<212> DNA

<213> artificial sequence

<220>

<223> CD19xVL3VH5 HLLH

<400> 390

cagggtgcagc tgcagcagtc tggggctgag ctggtgaggc ctgggtcctc agtgaagatt	60
tcctgcaagg cttctggcta tgcattcagt agctactgga tgaactgggt gaagcagagg	120
cctggacagg gtcttgagtg gattggacag atttggcctg gagatggtga tactaactac	180
aatggaaagt tcaagggtaa agccactctg actgcagacg aatcctccag cacagcctac	240
atgcaactca gcagcctagc atctgaggac tctgcggtct atttctgtgc aagacgggag	300
actacgacgg taggccgtta ttactatgct atggactact ggggcccaagg gaccacggtc	360
accgtctcct ccggtggtgg tggttctggc ggcggcggct ccggtggtgg tggttctgat	420

atccagctga cccagctctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc 480
 tcctgcaagg ccagccaaag tgttgattat gatggtgata gttatttgaa ctggtaccaa 540
 cagattccag gacagccacc caaactcctc atctatgatg catccaatct agtttctggg 600
 atcccaccca ggtttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct 660
 gtggagaagg tggatgctgc aacctatcac tgtcagcaaa gtactgagga tccgtggacg 720
 ttcggtggag ggaccaagct cgagatcaaa tccggaggtg gtggatccga cattgtactg 780
 acccagtctc cagcaactct gtctctgtct ccaggggagc gtgccaccct gacctgcaga 840
 gccagttcaa gtgtaagtta catgaactgg taccagcaga agccgggcaa ggcacccaaa 900
 agatggattt atgacacatc caaagtggct tctggagtcc ctgctcgctt cagtggcagt 960
 gggctctggga ccgactactc tctcacaatc aacagcttgg aggctgaaga tgctgccact 1020
 tattactgcc aacagtggag tagtaaccog ctcacgttcg gtggcgggac caaggtggag 1080
 atcaaaggcg aaggtactag tactggttct ggtggaagtg gaggttcagg tggagcagac 1140
 gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg 1200
 tcctgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca 1260
 cctggacagg gtctggaatg gattggatac attaatccta gccgtggtta tactaattac 1320
 gcagacagcg tcaagggccg cttcacaatc actacagaca aatccaccag cacagcctac 1380
 atggaactga gcagcctgcg ttctgaggac actgcaacct attactgtgc aagatattat 1440
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcacctg ctctctca 1497

<210> 391

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> CD19xVL3VH5 HLLH

<400> 391

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
 1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
 20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
130 135 140

Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
145 150 155 160

Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu
165 170 175

Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
180 185 190

Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser
195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val
210 215 220

Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr
225 230 235 240

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
260 265 270

Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
275 280 285

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
 290 295 300

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 305 310 315 320

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
 325 330 335

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
 340 345 350

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
 355 360 365

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
 370 375 380

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 385 390 395 400

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
 405 410 415

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 420 425 430

Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe
 435 440 445

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 450 455 460

Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Tyr Tyr
 465 470 475 480

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 485 490 495

Val Ser Ser

<211> 1497
<212> DNA
<213> artificial sequence

<220>
<223> CD19xVH7VL1 HLHL

<400> 392
caggtgcagc tgcagcagtc tggggctgag ctggtgaggc ctgggtcctc agtgaagatt 60
tcctgcaagg cttctggcta tgcattcagt agctactgga tgaactgggt gaagcagagg 120
cctggacagg gtcttgagtg gattggacag atttggcctg gagatggtga tactaactac 180
aatggaaagt tcaagggtaa agccactctg actgcagacg aatcctccag cacagcctac 240
atgcaactca gcagcctagc atctgaggac tctgcggtct atttctgtgc aagacgggag 300
actacgacgg taggcogtta ttactatgct atggactact ggggccaagg gaccacggtc 360
accgtctcct ccggtggtgg tggttctggc ggcggcggct ccggtggtgg tggttctgat 420
atccagctga ccagctctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc 480
tcctgcaagg ccagccaaag tgttgattat gatggtgata gttatttgaa ctggtaccaa 540
cagattccag gacagccacc caaactcctc atctatgatg catccaatct agtttctggg 600
atccccacca ggtttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct 660
gtggagaagg tggatgctgc aacctatcac tgtcagcaaa gtactgagga tccgtggacg 720
ttcggtgagg ggaccaagct cgagatcaaa tccggagggtg gtggatccga cgtccaactg 780
gtgcagtcag gggctgaagt gaaaaaacct ggggcctcag tgaagggtgtc ctgcaaggct 840
tctggctaca cctttactag gtacacgatg cactgggtaa ggcaggcacc tggacagggt 900
ctggaatgga ttggatacat taatcctagc cgtgggtata ctaattacaa tcagaagttc 960
aaggaccgag tcacaatcac tacagacaaa tccaccagca cagcctacat ggaactgagc 1020
agcctgcgtt ctgaggacac tgcagtctat tactgtgcaa gatattatga tgatcattac 1080
tgccttgact actggggcca aggcaccacg gtcaccgtct cctcaggcga aggtactagt 1140
actggttctg gtggaagtgg aggttcaggt ggagcagacg acattcagat gaccagctct 1200
ccatctagcc tgtctgcac tgtcggggac cgtgtcacca tcacctgcag agccagtcaa 1260
agtgtaagtt acatgaactg gtaccagcag aagccgggca aggaccccaa aagatggatt 1320
tatgacacat ccaaagtggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg 1380
accgactact ctctcacaat caacagcttg gaggtgaag atgctgccac ttattactgc 1440
caacagtgga gtagtaaccc gtcacgttc ggtggcggga ccaaggtgga gatcaaa 1497

<210> 393
 <211> 499
 <212> PRT
 <213> artificial sequence

<220>
 <223> CD19xVH7VL1 HLHL

<400> 393

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
 1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
 20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
 65 70 75 80

Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95

Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
 100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
 115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
 130 135 140

Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
 145 150 155 160

Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu
 165 170 175

Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
 180 185 190

Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser

195	200	205
Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val 210 215 220		
Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr 225 230 235 240		
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser 245 250 255		
Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala 260 265 270		
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr 275 280 285		
Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile 290 295 300		
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe 305 310 315 320		
Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr 325 330 335		
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys 340 345 350		
Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly 355 360 365		
Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly 370 375 380		
Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Gln Met Thr Gln Ser 385 390 395 400		
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys 405 410 415		
Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro 420 425 430		

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 435 440 445

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 450 455 460

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 465 470 475 480

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 485 490 495

Glu Ile Lys

<210> 394
 <211> 1494
 <212> DNA
 <213> artificial sequence

<220>
 <223> CD19xVL1VH7 LHLH

<400> 394
 gatatccagc tgaccagtc tccagcttct ttggctgtgt ctctagggca gagggccacc 60
 atctcctgca aggccagcca aagtgttgat tatgatggtg atagttattt gaactggtac 120
 caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 180
 gggatcccac ccagggttag tggcagtggt tctgggacag acttcaccct caacatccat 240
 cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg 300
 acgttcggtg gagggaccaa gctcgagatc aaaggtggtg gtggttctgg cggcggcggc 360
 tccggtggtg gtggttctca ggtgcagctg cagcagctctg gggctgagct ggtgaggcct 420
 gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg 480
 aactgggtga agcagaggcc tggacagggt cttgagtga ttggacagat ttggcctgga 540
 gatggtgata ctaactacaa tggaaagttc aagggtaaag ccactctgac tgcagacgaa 600
 tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat 660
 ttctgtgcaa gacgggagac tacgacggta ggccgttatt actatgctat ggactactgg 720
 ggccaaggga ccacggtcac cgtctcctcc ggaggtggtg gatccgacat tcagatgacc 780
 cagtctccat ctagecctgtc tgcatctgtc ggggaccgtg tcaccatcac ctgcagagcc 840
 agtcaaagtg taagttacat gaactggtac cagcagaagc cgggcaaggc acccaaaaga 900

tggatttatg acacatccaa agtggcttct ggagtcctg ctgcttcag tggcagtggg 960
 tctgggaccg actactctct cacaatcaac agcttggagg ctgaagatgc tgccacttat 1020
 tactgccaac agtggagtag taacccgctc acgttcggtg gcgggaccaa ggtggagatc 1080
 aaaggcgaag gtactagtac tggttctggt ggaagtggag gttcaggtgg agcagacgac 1140
 gtccaactgg tgcagtcagg ggctgaagtg aaaaaacctg gggcctcagt gaaggtgtcc 1200
 tgcaaggctt ctggctacac ctttactagg tacacgatgc actgggtaag gcaggcacct 1260
 ggacagggtc tggaatggat tggatacatt aatcctagcc gtggttatac taattacaat 1320
 cagaagttca aggaccgcgt cacaatcact acagacaaat ccaccagcac agcctacatg 1380
 gaactgagca gcctgcgttc tgaggacact gcagtctatt actgtgcaag atattatgat 1440
 gatcattact gccttgacta ctggggccaa ggcaccacgg tcaccgtctc ctca 1494

<210> 395

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> CD19xVL1VH7 LHLH

<400> 395

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
 20 25 30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
 35 40 45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
 85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
 115 120 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
 130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
 145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
 165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
 180 185 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
 195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
 210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
 225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
 245 250 255

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
 260 265 270

Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn
 275 280 285

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp
 290 295 300

Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly
 305 310 315 320

Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp
 325 330 335

Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe
 340 345 350

Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly
 355 360 365

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val
 370 375 380

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
 385 390 395 400

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val
 405 410 415

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro
 420 425 430

Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr
 435 440 445

Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser
 450 455 460

Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp
 465 470 475 480

Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
 485 490 495

Ser Ser

<210> 396

<211> 1497

<212> DNA

<213> artificial sequence

<220>

<223> CD19xVL1VH7 HLLH

<400> 396

caggtgcagc tgcagcagtc tggggctgag ctggtgaggc ctgggtcctc agtgaagatt 60

tcttgcaagg cttctggcta tgcattcagt agctactgga tgaactgggt gaagcagagg 120

cctggacagg gtcttgagtg gattggacag atttggcctg gagatgggtga tactaactac 180

aatggaaagt tcaagggtaa agccactctg actgcagacg aatcctccag cacagcctac 240

atgcaactca gcagcctagc atctgaggac tctgcggtct atttctgtgc aagacgggag 300

actacgacgg taggcogtta ttactatgct atggactact ggggccaagg gaccacggtc 360
 accgtctcct ccggtggtgg tggttctggc ggcggcggct ccggtggtgg tggttctgat 420
 atccagctga ccagctctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc 480
 tcctgcaagg ccagccaaag tgttgattat gatggtgata gttatttgaa ctggtaccaa 540
 cagattccag gacagccacc caaactcctc atctatgatg catccaatct agtttctggg 600
 atcccaccca ggttttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct 660
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 ggggtctggga ccgactactc tctcacaatc aacagcttgg aggctgaaga tgctgccact 1020
 tattaactgcc aacagtggag tagtaacccg ctcacgttcg gtggcgggac caaggtggag 1080
 atcaaaggcg aaggtactag tactggttct ggtggaagtg gaggttcagg tggagcagac 1140
 gacgtccaac tgggtgcagtc aggggctgaa gtgaaaaaac ctggggcctc agtgaagggtg 1200
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 aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac 1380
 atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat 1440
 gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctctctca 1497

<210> 397

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> CD19xVL1VH7 HLLH

<400> 397

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
 1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
 20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
 65 70 75 80

Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95

Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
 100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
 115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
 130 135 140

Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
 145 150 155 160

Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu
 165 170 175

Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
 180 185 190

Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser
 195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val
 210 215 220

Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr
 225 230 235 240

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser
 245 250 255

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 260 265 270

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
 275 280 285

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
 290 295 300

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 305 310 315 320

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
 325 330 335

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
 340 345 350

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
 355 360 365

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
 370 375 380

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 385 390 395 400

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
 405 410 415

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 420 425 430

Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
 435 440 445

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 450 455 460

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr
 465 470 475 480

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
 485 490 495

Val Ser Ser

<210> 398
<211> 1497
<212> DNA
<213> artificial sequence

<220>

<223> CD19xVH7VL2 HLHL

<400> 398
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cctggacagg gtcttgagtg gattggacag atttggcctg gagatggtga tactaactac 180
aatggaaagt tcaagggtaa agccactctg actgcagacg aatcctccag cacagcctac 240
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accgtctcct ccggtggtgg tggttctggc ggcggcggct ccggtggtgg tggttctgat 420
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tcctgcaagg ccagccaaag tgttgattat gatggtgata gttatttgaa ctggtaccaa 540
cagattccag gacagccacc caaactcctc atctatgatg catccaatct agtttctggg 600
atcccacca ggtttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct 660
gtggagaagg tggatgctgc aacctatcac tgtcagcaaa gtactgagga tccgtggacg 720
ttcgggtggag ggaccaagct cgagatcaaa tccggagggtg gtggatccga cgtccaactg 780
gtgcagtcag gggctgaagt gaaaaaacct ggggcctcag tgaagggtgc ctgcaaggct 840
tctggctaca cctttactag gtacacgatg cactgggtaa ggcaggcacc tggacagggt 900
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tgccttgact actggggcca aggcaccacg gtcaccgtct cctcaggcga aggtactagt 1140
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ccagcaactc tgtctctgtc tccaggggag cgtgccaccc tgagctgcag agccagtcaa 1260
agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcacccaa aagatggatt 1320
tatgacacat ccaaagtggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg 1380
accgactact ctctcacaat caacagcttg gaggtgaag atgctgccac ttattactgc 1440

caacagtgga gtagtaaccc gctcacgttc ggtggcgaggga ccaaggtgga gatcaaa 1497

<210> 399

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> CD19xVH7VL2 HLHL

<400> 399

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
130 135 140

Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
145 150 155 160

Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu
165 170 175

Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr

180	185	190
Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser 195 200 205		
Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val 210 215 220		
Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr 225 230 235 240		
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser 245 250 255		
Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala 260 265 270		
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr 275 280 285		
Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile 290 295 300		
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe 305 310 315 320		
Lys Asp Arg Val Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr 325 330 335		
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys 340 345 350		
Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly 355 360 365		
Thr Thr Val Thr Val Ser Ser Gly Glu Gly Thr Ser Thr Gly Ser Gly 370 375 380		
Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser 385 390 395 400		
Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys 405 410 415		

Arg Ala Ser Gln Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 420 425 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 435 440 445

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 450 455 460

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 465 470 475 480

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 485 490 495

Glu Ile Lys

<210> 400
 <211> 1494
 <212> DNA
 <213> artificial sequence

<220>
 <223> CD19xVL2VH7 LHLH

<400> 400
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 caacagattc caggacagcc acccaaactc ctcatctatg atgcatcaa tctagtttct 180
 gggatccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatcat 240
 cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg 300
 acgttcggtg gagggaccaa gctcgagatc aaaggtggtg gtggttctgg cggcggcggc 360
 tccggtggtg gtggttctca ggtgcagctg cagcagctctg gggctgagct ggtgaggcct 420
 gggctctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg 480
 aactgggtga agcagaggcc tggacagggt cttgagtga ttggacagat ttggcctgga 540
 gatggtgata ctaactacaa tggaaagttc aagggtaaag ccactctgac tgcagacgaa 600
 tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat 660
 ttctgtgcaa gacgggagac tacgacggtg ggccgttatt actatgctat ggactactgg 720
 ggccaaggga ccacggtcac cgtctcctcc ggaggtggtg gatccgacat tgtactgacc 780

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cagtctccag caactctgtc tctgtctcca ggggagcgtg ccaccctgag ctgcagagcc 840
agtcaaagtg taagttacat gaactggtac cagcagaagc cgggcaaggc acccaaaaga 900
tggatttatg acacatccaa agtggcttct ggagtccttg ctgccttcag tggcagtggg 960
tctgggaccg actactctct cacaatcaac agcttgaggg ctgaagatgc tgccacttat 1020
tactgccaac agtggagtag taaccgcgtc acgttcggtg gcgggaccaa ggtggagatc 1080
aaaggcgaag gtactagtag tggttctggt ggaagtggag gttcaggtgg agcagacgac 1140
gtccaactgg tgcagtcagg ggctgaagtg aaaaaacctg gggcctcagt gaaggtgtcc 1200
tgcaaggctt ctggctacac ctttactagg tacacgatgc actgggtaag gcaggcacct 1260
ggacagggtc tggaatggat tggatacatt aatcctagcc gtggttatac taattacaat 1320
cagaagttca aggaccggt cacaatcact acagacaaat ccaccagcac agcctacatg 1380
gaactgagca gcctgcgttc tgaggacact gcagtctatt actgtgcaag atattatgat 1440
gatcattact gccttgacta ctggggccaa ggcaccacgg tcaccgtctc ctca 1494

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<210> 401

<211> 498

<212> PRT

<213> artificial sequence

<220>

<223> CD19xVL2VH7 LHLH

<400> 401

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Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1           5           10           15

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Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
          20           25           30

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```

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
          35           40           45

```

```

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
          50           55           60

```

```

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65           70           75           80

```

```

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
          85           90           95

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Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
 115 120 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
 130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
 145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
 165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
 180 185 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
 195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
 210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
 225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
 245 250 255

Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu
 260 265 270

Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met Asn
 275 280 285

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp
 290 295 300

Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly
 305 310 315 320

Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp
 325 330 335

Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe
 340 345 350

Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly
 355 360 365

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val
 370 375 380

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
 385 390 395 400

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val
 405 410 415

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro
 420 425 430

Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr
 435 440 445

Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser
 450 455 460

Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp
 465 470 475 480

Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
 485 490 495

Ser Ser

<210> 402

<211> 1497

<212> DNA

<213> artificial sequence

<220>

<223> CD19xVL2VH7 HLLH

<400> 402

caggtgcagc tgcagcagtc tggggctgag ctggtgaggc ctgggtcctc agtgaagatt 60

tcctgcaagg cttctggcta tgcattcagt agctactgga tgaactgggt gaagcagagg 120

cctggacagg gtcttgagtg gattggacag atttggcctg gagatggtga tactaactac 180

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aatggaaagt tcaagggtaa agccactctg actgcagacg aatcctccag cacagcctac      240
atgcaactca gcagcctagc atctgaggac tctgcggtct atttctgtgc aagacgggag      300
actacgacgg taggcogtta ttactatgct atggactact ggggccaagg gaccacggtc      360
accgtctcct ccggtggtgg tggttctggc ggcggcggct ccggtggtgg tggttctgat      420
atccagctga ccagctctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc      480
tcttgcaagg ccagccaaag tggtgattat gatggtgata gttatttgaa ctggtaccaa      540
cagattocag gacagccacc caaactcctc atctatgatg catccaatct agtttctggg      600
atcccaccca ggttttagtgg cagtgggtct gggacagact tcacctcaa catccatcct      660
gtggagaagg tggatgctgc aacctatcac tgtcagcaaa gtactgagga tccgtggacg      720
ttcgggtggag ggaccaagct cgagatcaaa tccggaggtg gtggatccga cattgtactg      780
accagctctc cagcaactct gtctctgtct ccaggggagc gtgccaccct gagctgcaga      840
gccagtcaaa gtgtaagtta catgaactgg taccagcaga agccgggcaa ggcacccaaa      900
agatggattt atgacacatc caaagtggct tctggagtcc ctgctcgctt cagtggcagt      960
gggtctggga ccgactactc tctcacaatc aacagcttgg aggctgaaga tgctgccact     1020
tattactgcc aacagtggag tagtaacccg ctcacgttcg gtggcgggac caaggtggag     1080
atcaaaggcg aaggtactag tactggttct ggtggaagtg gaggttcagg tggagcagac     1140
gacgtccaac tggtgacgtc aggggctgaa gtgaaaaaac ctggggcctc agtgaaggtg     1200
tcttgcaagg cttctggcta cacctttact aggtacacga tgcactgggt aaggcaggca     1260
cctggacagg gtctggaatg gattggatac attaatccta gccgtgggta tactaattac     1320
aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac     1380
atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat     1440
gatgatcatt actgccttga ctactggggc caaggcacca cggtcacogt ctctca      1497

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<210> 403

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> CD19xVL2VH7 HLLH

<400> 403

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
 1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
130 135 140

Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
145 150 155 160

Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu
165 170 175

Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
180 185 190

Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser
195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val
210 215 220

Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr
225 230 235 240

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 260 265 270

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
 275 280 285

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
 290 295 300

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 305 310 315 320

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
 325 330 335

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
 340 345 350

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
 355 360 365

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
 370 375 380

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 385 390 395 400

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
 405 410 415

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 420 425 430

Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
 435 440 445

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 450 455 460

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr
 465 470 475 480

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr

485

490

495

Val Ser Ser

<210> 404

<211> 1497

<212> DNA

<213> artificial sequence

<220>

<223> CD19xVH7VL3 HLHL

<400> 404

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cctggacagg gtcttgagtg gattggacag atttggcctg gagatggatga tactaactac	180
aatggaaagt tcaagggtaa agccactctg actgcagacg aatcctccag cacagcctac	240
atgcaactca gcagcctagc atctgaggac tctgcggtct atttctgtgc aagacgggag	300
actacgacgg tagggcgtta ttactatgct atggactact ggggcccaagg gaccacggtc	360
accgtctcct ccgggtggtgg tggttctggc ggcggcggct ccgggtggtgg tggttctgat	420
atccagctga cccagtctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc	480
tcctgcaagg ccagccaaag tgttgattat gatggtgata gttatttgaa ctggtaccaa	540
cagattccag gacagccacc caaactcctc atctatgatg catccaatct agtttctggg	600
atcccacca ggttttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct	660
gtggagaagg tggatgctgc aacctatcac tgtcagcaaa gtactgagga tccgtggacg	720
ttcgggtggag ggaccaagct cgagatcaaa tccggagggtg gtggatccga cgtccaactg	780
gtgcagtcag gggctgaagt gaaaaaacct ggggcctcag tgaagggtgc ctgcaaggct	840
tctggctaca cttttactag gtacacgatg cactgggtaa ggcaggcacc tggacagggt	900
ctggaatgga ttggatacat taatcctagc cgtgggtata ctaattacaa tcagaagttc	960
aaggaccgcg tcacaatcac tacagacaaa tccaccagca cagcctacat ggaactgagc	1020
agcctgcgtt ctgaggacac tgcagtctat tactgtgcaa gatattatga tgatcattac	1080
tgccttgact actggggcca aggcaccacg gtcaccgtct cctcaggcga aggtactagt	1140
actggttctg gtggaagtgg aggttcaggt ggagcagacg acattgtact gaccagttct	1200
ccagcaactc tgtctctgtc tccaggggag cgtgccaccc tgacctgcag agccagttca	1260
agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcacccaa aagatggatt	1320

tatgacacat ccaaagtggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg 1380

accgactact ctctcacaat caacagcttg gaggtgaag atgctgccac ttattactgc 1440

caacagtgga gtagtaaccc gctcacgttc ggtggcgga ccaaggtgga gatcaaa 1497

<210> 405

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> CD19xVH7VL3 HLHL

<400> 405

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
130 135 140

Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
145 150 155 160

Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu

165

Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Ile Val Leu Thr Gln Ser
385 390 395 400

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys
 405 410 415

Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 420 425 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 435 440 445

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
 450 455 460

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
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Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 485 490 495

Glu Ile Lys

<210> 406
 <211> 1494
 <212> DNA
 <213> artificial sequence

<220>
 <223> CD19xVL3VH7 LHLH

<400> 406
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 caacagattc caggacagcc acccaaactc ctcatctatg atgcatcaa tctagtttct 180
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 cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg 300
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 gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg 480
 aactgggtga agcagaggcc tggacagggt cttgagtgga ttggacagat ttggcctgga 540
 gatggtgata ctaactacaa tggaaagttc aagggtaaag ccactctgac tgcagacgaa 600
 tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat 660

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cagtctccag caactctgtc tctgtctcca ggggagcgtg ccaccctgac ctgcagagcc      840
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tctgggaccg actactctct cacaatcaac agcttggagg ctgaagatgc tgccacttat     1020
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aaaggcgaag gtactagtac tggttctggt ggaagtggag gttcaggtgg agcagacgac     1140
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tgcaaggctt ctggctacac ctttactagg tacacgatgc actgggtaag gcaggcacct     1260
ggacagggtc tggaatggat tggatacatt aatcctagcc gtggttatac taattacaat     1320
cagaagttca aggaccgctt cacaatcact acagacaaat ccaccagcac agcctacatg     1380
gaactgagca gcctgcgttc tgaggacact gcagtctatt actgtgcaag atattatgat     1440
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<210> 407
 <211> 498
 <212> PRT
 <213> artificial sequence

<220>
 <223> CD19xVL3VH7 LHLH

<400> 407

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Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
 20 25 30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
 35 40 45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
115 120 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
130 135 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
145 150 155 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
165 170 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
180 185 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
210 215 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp
245 250 255

Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu
260 265 270

Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met Asn
275 280 285

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp
290 295 300

Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly
305 310 315 320

Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp
 325 330 335

Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe
 340 345 350

Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr Gly
 355 360 365

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu Val
 370 375 380

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
 385 390 395 400

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val
 405 410 415

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro
 420 425 430

Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr
 435 440 445

Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser
 450 455 460

Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp
 465 470 475 480

Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
 485 490 495

Ser Ser

<210> 408
 <211> 1497
 <212> DNA
 <213> artificial sequence

<220>
 <223> CD19xVL3VH7 HLLH

<400> 408
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cctggacagg gtcttgagtg gattggacag atttggcctg gagatggtga tactaactac 180
aatggaaagt tcaagggtaa agccactctg actgcagacg aatcctccag cacagcctac 240
atgcaactca gcagcctagc atctgaggac tctgcggtct atttctgtgc aagacgggag 300
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accgtctcct ccggtgggtg tggttctggc ggcggcggct ccggtgggtg tggttctgat 420
atccagctga cccagtctcc agcttctttg gctgtgtctc tagggcagag ggccaccatc 480
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cagattccag gacagccacc caaactctc atctatgatg catccaatct agtttctggg 600
atcccacca ggttttagtgg cagtgggtct gggacagact tcaccctcaa catccatcct 660
gtggagaagg tggatgctgc aacctatcac tgtcagcaaa gtactgagga tccgtggacg 720
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atcaaaggcg aaggtactag tactggttct ggtggaagtg gaggttcagg tggagcagac 1140
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aatcagaagt tcaaggaccg cgtcacaatc actacagaca aatccaccag cacagcctac 1380
atggaactga gcagcctgcg ttctgaggac actgcagtct attactgtgc aagatattat 1440
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<210> 409

<211> 499

<212> PRT

<213> artificial sequence

<220>

<223> CD19xVL3VH7 HLLH

<400> 409

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Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
130 135 140

Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
145 150 155 160

Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu
165 170 175

Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
180 185 190

Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser
195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val
210 215 220

Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr
225 230 235 240

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser
 245 250 255

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 260 265 270

Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
 275 280 285

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
 290 295 300

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 305 310 315 320

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
 325 330 335

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
 340 345 350

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Glu Gly Thr Ser Thr
 355 360 365

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ala Asp Asp Val Gln Leu
 370 375 380

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 385 390 395 400

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
 405 410 415

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 420 425 430

Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
 435 440 445

Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 450 455 460

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr

465

470

475

480

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
485 490 495

Val Ser Ser